GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:30:12 ; Search time 50 Seconds
(without alignments)
765.018 Million cell updates/sec

Title: US-10-727-619-2
Perfect score: 2381
Sequence: 1 MSAVLLLALLGFILPLPGVQ.....WGVGLALAPALWWGVVCPSC 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2381	100.0	437	2	US-09-830-189C-2	Sequence 2, Appli
2	2381	100.0	437	2	US-09-991-181-355	Sequence 355, App
3	2381	100.0	437	2	US-09-990-444-355	Sequence 355, App
4	2381	100.0	437	2	US-10-033-301-16	Sequence 16, Appl
5	2381	100.0	437	2	US-09-997-333-355	Sequence 355, App
6	2381	100.0	437	2	US-09-992-598-355	Sequence 355, App
7	2381	100.0	437	2	US-10-033-435-16	Sequence 16, Appl
8	2381	100.0	437	2	US-09-989-735-355	Sequence 355, App
9	2381	100.0	437	3	US-09-989-726-355	Sequence 355, App
10	2381	100.0	437	3	US-09-997-514-355	Sequence 355, App
11	2381	100.0	437	3	US-09-989-728-355	Sequence 355, App
12	2381	100.0	437	3	US-09-997-349-355	Sequence 355, App
13	2381	100.0	437	3	US-09-997-653-355	Sequence 355, App
14	2381	100.0	437	3	US-09-989-293A-355	Sequence 355, App
15	2362	99.2	437	2	US-09-073-569-2	Sequence 2, Appli
16	438	18.4	81	2	US-09-621-976-4256	Sequence 4256, Ap
17	134.5	5.6	2050	1	US-08-347-594A-2	Sequence 2, Appli
18	131.5	5.5	819	2	US-10-094-749-1690	Sequence 1690, Ap
19	131.5	5.5	2813	2	US-09-381-261A-1	Sequence 1, Appli
20	128.5	5.4	212	2	US-09-886-319A-37	Sequence 37, Appl
21	128	5.4	1404	1	US-08-400-159-2	Sequence 2, Appli
22	128	5.4	1404	2	US-08-611-729A-2	Sequence 2, Appli
23	128	5.4	1404	2	US-09-195-524-2	Sequence 2, Appli
24	127.5	5.4	1964	2	US-09-467-997-1	Sequence 1, Appli
25	123	5.2	721	2	US-08-872-855-7	Sequence 7, Appli
26	121.5	5.1	606	3	US-10-029-840A-6	Sequence 6, Appli
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39	119.5	5.0	833	2	US-09-448-868-5	Sequence 5, Appli
40	119.5	5.0	833	2	US-10-226-296-5	Sequence 5, Appli
41	119	5.0	346	2	US-09-991-181-197	Sequence 197, App
42	119	5.0	346	2	US-09-990-444-197	Sequence 197, App
43	119	5.0	346	2	US-09-997-333-197	Sequence 197, App
44	119	5.0	346	2	US-09-992-598-197	Sequence 197, App
45	119	5.0	346	2	US-09-989-735-197	Sequence 197, App

ALIGNMENTS

RESULT 1
US-09-830-189C-2
; Sequence 2, Application US/09830189C
; Patent No. 6686153
; GENERAL INFORMATION:
; APPLICANT: PAHL, HEIKE
; TITLE OF INVENTION: PRV-1 AND THE USE THEREOF
; FILE REFERENCE: LEDER-1
; CURRENT APPLICATION NUMBER: US/09/830,189C
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/EP99/07238
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 198 49 044.5
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-189C-2

Query Match 100.0%; Score 2381; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e-213;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-991-181-355
; Sequence 355, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C53
;  CURRENT APPLICATION NUMBER: US/09/991,181
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/091978
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e-213;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-990-444-355
; Sequence 355, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

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RESULT 4
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; Sequence 16, Application US/10033301
; Patent No. 6930172
; GENERAL INFORMATION:
;  APPLICANT: Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Roy,Margaret Ann
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2930R1C6
;  CURRENT APPLICATION NUMBER: US/10/033,301
;  CURRENT FILING DATE:  2001-12-27
;  PRIOR APPLICATION NUMBER: 60/095,325
;  PRIOR FILING DATE: 1998-08-04
;  PRIOR APPLICATION NUMBER: 60/112,851
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;  PRIOR APPLICATION NUMBER: 60/187,202
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;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: 1999-06-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28634
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: PCT/US99/28551
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
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;  NUMBER OF SEQ ID NOS: 38
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-033-301-16

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  Best Local Similarity   100.0%;  Pred. No. 8.3e-213;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
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; Patent No. 6953836
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
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;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
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;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
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;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C27
;  CURRENT APPLICATION NUMBER: US/09/997,333
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Query Match 100.0%; Score 2381; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e-213;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
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Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
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Qy        421 GLALAPALWWGVVCPSC 437
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Db        421 GLALAPALWWGVVCPSC 437
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RESULT 6
US-09-992-598-355
; Sequence 355, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598

; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

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Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
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Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

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Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
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Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
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Qy        421 GLALAPALWWGVVCPSC 437
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Db        421 GLALAPALWWGVVCPSC 437


RESULT 7
US-10-033-435-16
; Sequence 16, Application US/10033435
; Patent No. 6969758
; GENERAL INFORMATION:
;  APPLICANT: Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Roy,Margaret Ann
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2930R1C5
;  CURRENT APPLICATION NUMBER: US/10/033,435
;  CURRENT FILING DATE:  2001-12-27
;  PRIOR APPLICATION NUMBER: 60/095,325
;  PRIOR FILING DATE: 1998-08-04
;  PRIOR APPLICATION NUMBER: 60/112,851
;  PRIOR FILING DATE: 1998-12-16
;  PRIOR APPLICATION NUMBER: 60/113,145
;  PRIOR FILING DATE: 1998-12-16
;  PRIOR APPLICATION NUMBER: 60/113,511
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;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/115,565
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/115,733
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;  PRIOR APPLICATION NUMBER: 60/119,341
;  PRIOR FILING DATE: 1999-02-09
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;  PRIOR APPLICATION NUMBER: 60/119,965
;  PRIOR FILING DATE: 1999-02-12
;  PRIOR APPLICATION NUMBER: 60/162,506
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: 60/170,262
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/187,202
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
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;  PRIOR APPLICATION NUMBER: PCT/US99/28634
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;  PRIOR APPLICATION NUMBER: PCT/US00/04414
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;  PRIOR APPLICATION NUMBER: PCT/US00/15264
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;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 16
;   LENGTH: 437
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-033-435-16

  Query Match           100.0%;  Score 2381;  DB 2;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-213;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
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Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
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Db          61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy         121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
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Qy         181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
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Qy         301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
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Qy         361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
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Qy         421 GLALAPALWWGVVCPSC 437
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RESULT 8
US-09-989-735-355
; Sequence 355, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C61
;  CURRENT APPLICATION NUMBER: US/09/989,735
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 2; Length 437;
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C60
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;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
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;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
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;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C46
;  CURRENT APPLICATION NUMBER: US/09/997,514
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e-213;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
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; Patent No. 7029873
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
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;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
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;  APPLICANT:  Gerritsen,Mary E.
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;  APPLICANT:  Grimaldi,J.Christopher
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;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C72
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
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RESULT 12
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; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; CURRENT FILING DATE: 2001-11-15

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;  PRIOR FILING DATE: 1998-07-09

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;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
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;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
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;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C38
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
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Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
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;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
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;  TITLE OF INVENTION:  Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 8.3e-213;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 2, Application US/09073569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal

US-09-073-569-2

Query Match 99.2%; Score 2362; DB 2; Length 437;
Best Local Similarity 99.5%; Pred. No. 4.9e-211;
Matches 435; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Job time : 52 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 10:48:16 ; Search time 451 Seconds
(without alignments)
4612.445 Million cell updates/sec

Title: US-10-727-619-1
Perfect score: 1600
Sequence: 1 aaaagcagaaagagattacc.....ctgataatacagaccctgtc 1600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 844069 seqs, 650066433 residues

Total number of hits satisfying chosen parameters: 1688138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	928.8	58.1	986	8	US-11-266-748A-452990	Sequence 452990,
	3	883	55.2	1000	8	US-11-266-748A-295073	Sequence 295073,
c	4	883	55.2	1000	8	US-11-266-748A-346502	Sequence 346502,
c	5	874.4	54.6	1000	8	US-11-266-748A-215833	Sequence 215833,
	6	874.4	54.6	1000	8	US-11-266-748A-237848	Sequence 237848,
	7	627.4	39.2	654	8	US-11-266-748A-2984	Sequence 2984, Ap
	8	597.8	37.4	749	8	US-11-266-748A-17659	Sequence 17659, A
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	17	72.4	4.5	1092	8	US-11-266-748A-451386	Sequence 451386,
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	38	38.8	2.4	2457	7	US-11-218-305-16443	Sequence 16443, A
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	40	38.8	2.4	5862	8	US-11-264-243-17	Sequence 17, Appl
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ALIGNMENTS

RESULT 1
US-11-266-748A-369611
; Sequence 369611, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
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; SEQ ID NO 369611
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (833)..(834)
; OTHER INFORMATION: n is a, c, g, or t
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Best Local Similarity 96.9%; Pred. No. 1.8e-246;

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RESULT 2
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; Sequence 452990, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
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;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
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US-11-266-748A-452990

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  Matches  956;  Conservative    0;  Mismatches   30;  Indels    1;  Gaps    1;

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Db        806 GATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC 747

Qy        272 CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTC 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTC 687

Qy        332 CTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT 627

Qy        392 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTAT 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        626 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTAT 567

Qy        452 GGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTA 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 GGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTA 507

Qy        512 TGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATG 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 TGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATG 447

Qy        572 CATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTAT 631
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        446 CATGCCCCAGCCAGTTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTAT 387

Qy        632 GACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGAC 691
              ||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||
Db        386 GACTGAGAACTGCGATATGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGAC 327

Qy        692 ACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGA 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 ACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGA 267

Qy        752 GGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 AGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCT 207

Qy        812 GGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCA 871
              |||||||   |||||||||||||||||||||||||| | |||||||   |      ||
Db        206 GGTGGGGGACAAAGGCTGCAGCACTGTTGGGGCTCAAATTNCCCAGAAAGACNNACATCA 147

Qy        872 CTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTG 931
              ||||||||||||||||||||||   | ||||||||||||||||||||||||||||||||||
Db        146 CTCAGCCCCTCCTGGGGTGCTTTGTGGCTCCTATACCCACTTCTGCTCCTCGGACCTGTG 87

Qy        932 CAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGT 991
              |||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||
Db         86 CAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCT-CTCCAGCTGCCCCTGT 28

Qy        992 CCCAGGAGACCGGCAGTGTCCTACCTG 1018
              |||||||||| |      |||||||||
Db         27 CCCAGGAGACGGCAGTGTTCCTACCTG 1


RESULT 3
US-11-266-748A-295073
; Sequence 295073, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 295073
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-295073

  Query Match             55.2%;  Score 883;  DB 8;  Length 1000;
  Best Local Similarity   94.3%;  Pred. No. 8.3e-234;
  Matches  938;  Conservative    0;  Mismatches   55;  Indels    2;  Gaps    2;

Qy        606 ACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACC 665
              |||||||||||||||||||||||||||||||||||||||||| ||| ||||||| ||||||||
Db          1 ACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCGATATGAAAGATGTTCTGACC 60

Qy        666 TGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGG 725
              |||||||||||||||||| | | ||  || | |||||||  | ||||||||||||||||||
Db         61 TGTCATCGGGGGACCACCTTGAAGAAGCAGGAAAACTTGAGTAAAGAACCCACTGATTGG 120

Qy        726 ACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTC 785
              ||||||| |||||||||| ||||||||||||||||||||||||||||||| ||||||||||
Db        121 GCCACATCTAATACCGAGACGTGCGAGGTGGGGCAGGTGTGTCAGGAGATGCTGCTGCTC 180

Qy        786 ATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCT 845
              |||||||||||||||||||||||||||||| |||  || |||||||| ||||||||||||
Db        181 ATAGATGTAGGACTCACATCAACCCTGGTGGCGACCTAAAGCTGCAGCGCTGTTGGGGCT 240

Qy        846 CAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTAT 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTAT 300

Qy        906 ACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAAC 965
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAAC 360

Qy        966 TCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAG 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAG 420

Qy       1026 CCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCAT 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCAT 480

Qy       1086 TGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAG 1145
              |||||||||||||||||||||||||||||||||||||| |||||| ||||||||||||||
Db        481 TGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGACCACCAGAATGAGCATTCAG 540

Qy       1146 GGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTC 1205
              ||||| |||||||||||||||||| ||||||||||||||||||||||||| |||||||||
Db        541 GGCTGTGTGGCCCAACCTTCCAGCTCCTTGTTGAACCACACCAGACAAATTGGGATCTTC 600

Qy       1206 TCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCT 1265
              |||| | |||||||| |||||| || ||||||||||||||||||||||||||||||||||
Db        601 TCTGTGTGTGAGAAGGGTGATGAGCCGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCT 660

Qy       1266 GAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGG 1325
              | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGGGCCTGGAGTGTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGG 720

Qy       1326 GGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACC 1385
              |||| |||||||||||||||||||| ||| ||||||||||||||||||||||||| |||
Db        721 GGAGCGGTTTGCCCTTCCTGCTAACTCCATTTCCCCCACGATTCTTCACCGCTGCTCACC 780

Qy       1386 ACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTT- 1444
              | |||||||||||  ||  ||  ||  |||||||||||||||||||||||||||||| |||
Db        781 A-CCACACTCAACCGTCCCTTGTGCTTGTAACCTAATGGCCTTGGACACCAGATTATTTC 839

Qy       1445 CCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACA 1504
              ||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||| |
Db        840 CCCATCCTGTCCATGAATCATCTTCCCCACACATAATCATTCATATCTACTCACCTAATA 899

Qy       1505 GCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAG 1564
              |||||||||||||||||||||||||| |||||||||||| |||||||||||| ||||||
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Db        900 GCAACACTGGGGAGAGCCTGGAGCAGCCGGACTTGCCCTGTGGGAGAGGGGACACTGGAG 959

Qy       1565 GAGTGGCTGCATGTATCTGATAATACAGACCCTGT 1599
              ||||||||||||||| |||||||||| |||||||||
Db        960 GAGTGGCTGCATGTGTCTGATAATAAAGACCCTGT 994


RESULT 4
US-11-266-748A-346502/c
; Sequence 346502, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 346502
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-346502

  Query Match             55.2%;  Score 883;  DB 8;  Length 1000;
  Best Local Similarity   94.3%;  Pred. No. 8.3e-234;
  Matches  938;  Conservative    0;  Mismatches   55;  Indels    2;  Gaps    2;

Qy         606 ACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACC 665
               |||||||||||||||||||||||||||||||||||||||||| ||| ||||||| ||||||||
Db        1000 ACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCGATATGAAAGATGTTCTGACC 941

Qy         666 TGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGG 725
               |||||||||||||||||| | | ||  || | |||||||  | ||||||||||||||||||
Db         940 TGTCATCGGGGGACCACCTTGAAGAAGCAGGAAAACTTGAGTAAAGAACCCACTGATTGG 881

Qy         726 ACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTC 785
               |||||||  |||||||||| |||||||||||||||||||||||||||||| ||||||||||
Db         880 GCCACATCTAATACCGAGACGTGCGAGGTGGGGCAGGTGTGTCAGGAGATGCTGCTGCTC 821

Qy         786 ATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCT 845
               |||||||||||||||||||||||||||||| |||  || ||||||||  ||||||||||||
Db         820 ATAGATGTAGGACTCACATCAACCCTGGTGGCGACCTAAAGCTGCAGCGCTGTTGGGGCT 761

Qy         846 CAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTAT 905
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         760 CAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTAT 701

Qy         906 ACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAAC 965
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         700 ACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAAC 641

Qy         966 TCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAG 1025
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         640 TCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAG 581

Qy        1026 CCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCAT 1085
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         580 CCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCAT 521

Qy        1086 TGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAG 1145
               |||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||||
Db         520 TGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGACCACCAGAATGAGCATTCAG 461

Qy        1146 GGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTC 1205
               ||||| |||||||||||||||||| |||||||||||||||||||||||| |||||||||
Db         460 GGCTGTGTGGCCCAACCTTCCAGCTCCTTGTTGAACCACACCAGACAAATTGGGATCTTC 401

Qy        1206 TCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCT 1265
               |||| | |||||||| ||||||| || ||||||||||||||||||||||||||||||||||
Db         400 TCTGTGTGTGAGAAGGGTGATGAGCCGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCT 341

Qy        1266 GAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGG 1325
               | |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         340 GGGGGCCTGGAGTGTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGG 281

Qy        1326 GGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACC 1385
               |||| |||||||||||||||||||| ||| |||||||||||||||||||||||| |||
Db         280 GGAGCGGTTTGCCCTTCCTGCTAACTCCATTTCCCCCACGATTCTTCACCGCTGCTCACC 221

Qy        1386 ACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTT- 1444
               | |||||||||||  ||  ||  ||  |||||||||||||||||||||||||||| |||
Db         220 A-CCACACTCAACCGTCCCTTGTGCTTGTAACCTAATGGCCTTGGACACCAGATTATTC 162

Qy        1445 CCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACA 1504
               ||||| |||||||||||||||||||||||||||||||||| |||||||||||||||||| |
Db         161 CCCATCCTGTCCATGAATCATCTTCCCCACACATAATCATTCATATCTACTCACCTAATA 102

Qy        1505 GCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAG 1564
               |||||||||||||||||||||||| |||||||||||| |||||||||||| ||||||
Db         101 GCAACACTGGGGAGAGCCTGGAGCAGCCGGACTTGCCCTGTGGGAGAGGGGACACTGGAG 42

Qy        1565 GAGTGGCTGCATGTATCTGATAATACAGACCCTGT 1599
               |||||||||||||| |||||||||| |||||||||
Db          41 GAGTGGCTGCATGTGTCTGATAATAAAGACCCTGT 7


RESULT 5
US-11-266-748A-215833/c
; Sequence 215833, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
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;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 215833
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (48)..(48)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-215833

  Query Match           54.6%;  Score 874.4;  DB 8;  Length 1000;
  Best Local Similarity   98.9%;  Pred. No. 2e-231;
  Matches  889;  Conservative    1;  Mismatches    8;  Indels    1;  Gaps    1;

Qy        650 GAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCA 709
              |||||||||||||||||||||| |||||||||||||||||||||||| |||| |||||
Db        898 GAAAGATTTTCTGACCTGTCATC-GGGGACCACCATTATGACACACGGACACTTTGCTCA 840

Qy        710 AGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 AGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 780

Qy        770 GGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTG 829
              |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db        779 GGAGACGCTGCTGCTCCTAGATGTAGAACTCACATCAACCCTGGTGGGGACAAAAGGCTG 720

Qy        830 CAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGT 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 CAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGT 660

Qy        890 GCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG 600

Qy        950 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTG 1009
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        599 CAGCGTTCTGCTGTACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTG 540

Qy       1010 TCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCC 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 TCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCC 480

Qy       1070 CAGGGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCAC 1129
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 CAGGGGCACCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCAC 420

Qy       1130 CAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAG 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 CAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAG 360

Qy       1190 ACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCA 1249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 ACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCA 300

Qy       1250 TGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGC 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 TGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGC 240

Qy       1310 CCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTC 1369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTC 180

Qy       1370 TTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTG 1429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 TTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTG 120

Qy       1430 GACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATA 1489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 GACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATA 60

Qy       1490 TCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGG 1548
              |||||||||| |||||||||||||||||||||||||||||| |||:|||||||||||||
Db         59 TCTACTCACCTNACAGCAACACTGGGGAGAGCCTGGAGCAGCCGKACTTGCCCTATGGG 1

RESULT 6
US-11-266-748A-237848
; Sequence 237848, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 237848
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (953)..(953)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-237848

  Query Match           54.6%;  Score 874.4;  DB 8;  Length 1000;
  Best Local Similarity   98.9%;  Pred. No. 2e-231;
  Matches  889;  Conservative    1;  Mismatches    8;  Indels    1;  Gaps    1;

Qy        650 GAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCA 709
              |||||||||||||||||||||| |||||||||||||||||||||||| |||| |||||
Db        103 GAAAGATTTTCTGACCTGTCATC-GGGGACCACCATTATGACACACGGACACTTTGCTCA 161

Qy        710 AGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 221

Qy        770 GGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTG 829
              |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db        222 GGAGACGCTGCTGCTCCTAGATGTAGAACTCACATCAACCCTGGTGGGGACAAAAGGCTG 281

Qy        830 CAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGT 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 CAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGT 341

Qy        890 GCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 GCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG 401

Qy        950 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTG 1009
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        402 CAGCGTTCTGCTGTACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTG 461
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Qy       1010 TCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCC 1069
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 TCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCC 521

Qy       1070 CAGGGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCAC 1129
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 CAGGGGCACCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCAC 581

Qy       1130 CAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAG 1189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 CAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAG 641

Qy       1190 ACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCA 1249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 ACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCA 701

Qy       1250 TGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGC 1309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 TGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGC 761

Qy       1310 CCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTC 1369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 CCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTC 821

Qy       1370 TTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTG 1429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 TTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTG 881

Qy       1430 GACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATA 1489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 GACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATA 941

Qy       1490 TCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGG 1548
             |||||||||||| |||||||||||||||||||||||||||||| |||:|||||||||||||
Db        942 TCTACTCACCTNACAGCAACACTGGGGAGAGCCTGGAGCAGCCGKACTTGCCCTATGGG 1000
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RESULT 7
US-11-266-748A-2984
; Sequence 2984, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2984
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-2984

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  Query Match           39.2%;  Score 627.4;  DB 8;  Length 654;
  Best Local Similarity  99.8%;  Pred. No. 2.9e-163;
  Matches  628;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        941 CAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGA 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 CAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGA 85

Qy       1001 CCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAAT 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 CCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAAT 145

Qy       1061 GACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGG 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGG 205

Qy       1121 GCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAA 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAA 265

Qy       1181 CCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGC 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGC 325

Qy       1241 CTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCT 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCT 385

Qy       1301 GGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCC 1360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 GGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCC 445

Qy       1361 CCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTA 1420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 CCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTA 505

Qy       1421 ATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAA 1480
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        506 ATGGCCTTGGACACCAGATTCTTACCCATTCTGTCCATGAATCATCTTCCCCACACACAA 565

Qy       1481 TCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGC 1540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 TCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGC 625

Qy       1541 CCTATGGGAGAGGGGACGCTGGAGGAGTG 1569
              |||||||||||||||||||||||||||||
Db        626 CCTATGGGAGAGGGGACGCTGGAGGAGTG 654
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RESULT 8
US-11-266-748A-17659
; Sequence 17659, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03

```
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17659
;   LENGTH: 749
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-17659

  Query Match             37.4%;  Score 597.8;  DB 8;  Length 749;
  Best Local Similarity   99.5%;  Pred. No. 4.7e-155;
  Matches  610;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy        987 CCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGT 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGT 196

Qy       1047 GGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTACATTCAT 1106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTACATTCAT 256

Qy       1107 CTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCC 1166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCC 316

Qy       1167 AGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGAT 1226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGAT 376

Qy       1227 GTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACT 1286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACT 436

Qy       1287 TGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGC 1346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 TGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGC 496

Qy       1347 TAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCT 1406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 TAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCT 556

Qy       1407 GACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGAATCATC 1466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGAATCATC 616

Qy       1467 TTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGA 1526
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        617 TTCCCCACACACAATCATTCATATCTATTCACCTAACAGCAACACTGGGGAGAGCCTGGA 676

Qy       1527 GCATCCGGACTTGCCCTAT-GGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGAT 1585
              ||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        677 GCATCCGGACTTGCTCTATGGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGAT 736

Qy       1586 AATACAGACCCTG 1598
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Db        737 AATACAGACCCTG 749


RESULT 9
US-11-266-748A-54407
; Sequence 54407, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54407
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-54407

  Query Match             32.2%;  Score 516;  DB 8;  Length 549;
  Best Local Similarity   97.8%;  Pred. No. 1.6e-132;
  Matches  534;  Conservative    0;  Mismatches   10;  Indels    2;  Gaps    1;

Qy       1026 CCCCTTGGAACCTGTTCAAGTGGCTCCCCCCG--AATGACCTGCCCCAGGGGCGCCACTC 1083
              ||  |  ||| |||| ||||||||||||||||   ||||||||||||||||||||||||||
Db          4 CCGTTGCGAAGCTGTACAAGTGGCTCCCCCCGTATATGACCTGCCCCAGGGGCGCCACTC 63

Qy       1084 ATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTC 1143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTC 123

Qy       1144 AGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCT 1203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCT 183

Qy       1204 TCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGG 1263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 TCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGG 243

Qy       1264 CTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGT 1323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGT 303

Qy       1324 GGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA 1383
              |||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db        304 GGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGATGATGA 363

Qy       1384 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTT 1443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTT 423

Qy       1444 TCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAAC 1503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 ACCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAAC 483

Qy       1504 AGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGA 1563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGA 543

Qy       1564 GGAGTG 1569
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Db        544 GGAGTG 549


RESULT 10
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US-11-266-748A-368008
; Sequence 368008, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 368008
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-368008

  Query Match             4.6%;  Score 74;  DB 8;  Length 1037;
  Best Local Similarity   51.0%;  Pred. No. 3.1e-10;
  Matches  254;  Conservative    0;  Mismatches  235;  Indels    9;  Gaps    3;

Qy        719 TGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCT 778
              | | |||||||||  | |    ||||  || ||    |||    | || |||||  ||  |
Db        297 TAACTGGACCACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 356

Qy        779 GCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT 838
              ||  | ||  | | |||         || || |  |||  || || ||||||| | | |
Db        357 ACTAATAATTAAAGCAGGGACTGAGACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGA 416

Qy        839 TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGC 898
              ||||   | | ||   | |     |  |||||  | ||||| ||  || | ||| |
Db        417 AGGGG---AGGAGGCCATAACAATTGTCCAGCACTCTTCACCTCCCGGCCTGATCGTGAC 473

Qy        899 CTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCT 958
              ||||||  |   ||| |||          | | || |||         ||||          |
Db        474 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCTGTCTCAGTT 533

Qy        959 GCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTG 1018
                | | | |     |   |||| || ||||  ||  |  ||  || ||||| |||||
Db        534 TTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTCAACAACCCTCCATTGTCCAACCTG 593

Qy       1019 TGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGC 1078
              |||   | |  | || |||||||  ||||   | ||      |  |||| |||| ||  |
Db        594 TGT---GGCTTTGGGGACCTGTTTCAGTG---CTCCTTCTCTTCCCTGTCCCAATGGTAC 647

Qy       1079 CACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAG 1138
              ||||  || ||| | ||  |  || |  || | ||||||||  |      |     ||
Db        648 AACTCGATGCTATCAAGGAAAACTTGAGATCACTGGAGGTGGCATTGAGTCGTCTGTGGA 707

Qy       1139 CATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGG 1198
                |  | |||||    |||     |  | ||    || ||          | |  |  | ||
Db        708 GGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTTAGCAGTAGG 767

Qy       1199 GATCTTCTCTGCGCGTGA 1216
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              | | | || | | ||
Db        768 ACCCATGTTTGTGAGGGA 785


RESULT 11
US-11-266-748A-388965
; Sequence 388965, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 388965
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-388965

  Query Match             4.6%;  Score 74;  DB 8;  Length 1037;
  Best Local Similarity   51.0%;  Pred. No. 3.1e-10;
  Matches  254;  Conservative    0;  Mismatches  235;  Indels    9;  Gaps    3;

Qy        719 TGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCT 778
              | | |||||||||  | |    ||||  || ||    |||    | || |||||  ||  |
Db        297 TAACTGGACCACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 356

Qy        779 GCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT 838
              ||  | ||  | | |||         || || |  |||  || || ||||||| | | |
Db        357 ACTAATAATTAAAGCAGGGACTGAGACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGA 416

Qy        839 TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGC 898
              ||||   | | ||   | |     |  |||||  | ||||| ||  || | ||| |
Db        417 AGGGG---AGGAGGCCATAACAATTGTCCAGCACTCTTCACCTCCCGGCCTGATCGTGAC 473

Qy        899 CTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCT 958
              ||||||  |   ||| |||          | | || |||         ||||          |
Db        474 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCTGTCTCAGTT 533

Qy        959 GCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTG 1018
                | | | |     |   |||| || ||||  ||  |  ||  || ||||| |||||
Db        534 TTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTCAACAACCCTCCATTGTCCAACCTG 593

Qy       1019 TGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGC 1078
              |||   | |  | || |||||||  ||||   | ||      |  |||| |||| ||  |
Db        594 TGT---GGCTTTGGGGACCTGTTTCAGTG---CTCCTTCTCTTCCCTGTCCCAATGGTAC 647

Qy       1079 CACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAG 1138
              ||||  || ||| | ||  |  || |  || | ||||||||  |      |     ||
Db        648 AACTCGATGCTATCAAGGAAAACTTGAGATCACTGGAGGTGGCATTGAGTCGTCTGTGGA 707
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Qy       1139 CATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGG 1198
Db        708 GGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTTAGCAGTAGG 767

Qy       1199 GATCTTCTCTGCGCGTGA 1216
Db        768 ACCCATGTTTGTGAGGGA 785
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RESULT 12
US-11-266-748A-451387/c
; Sequence 451387, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 451387
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-451387

Query Match 4.6%; Score 74; DB 8; Length 1037;
Best Local Similarity 51.0%; Pred. No. 3.1e-10;
Matches 254; Conservative 0; Mismatches 235; Indels 9; Gaps 3;

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Qy        719 TGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCT 778
Db        741 TAACTGGACCACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 682

Qy        779 GCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT 838
Db        681 ACTAATAATTAAAGCAGGGACTGAGACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGA 622

Qy        839 TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGC 898
Db        621 AGGGG---AGGAGGCCATAACAATTGTCCAGCACTCTTCACCTCCCGGCCTGATCGTGAC 565

Qy        899 CTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCT 958
Db        564 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCTGTCTCAGTT 505

Qy        959 GCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTG 1018
Db        504 TTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTCAACAACCCTCCATTGTCCAACCTG 445

Qy       1019 TGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGC 1078
Db        444 TGT---GGCTTTGGGGACCTGTTTCAGTG---CTCCTTCTCTTCCCTGTCCCAATGGTAC 391
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Qy       1079 CACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAG 1138
Db        390 AACTCGATGCTATCAAGGAAAACTTGAGATCACTGGAGGTGGCATTGAGTCGTCTGTGGA 331

Qy       1139 CATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGG 1198
Db        330 GGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTTAGCAGTAGG 271

Qy       1199 GATCTTCTCTGCGCGTGA 1216
Db        270 ACCCATGTTTGTGAGGGA 253
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RESULT 13
US-11-266-748A-291309
; Sequence 291309, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 291309
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-291309

Query Match 4.6%; Score 73.2; DB 8; Length 1000;
Best Local Similarity 48.0%; Pred. No. 5e-10;
Matches 306; Conservative 0; Mismatches 323; Indels 9; Gaps 3;

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Qy        719 TGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCT 778
Db        141 TAACTGGACCACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 200

Qy        779 GCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT 838
Db        201 ACTAATAATTAAAGCAGGGACTGAGACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGA 260

Qy        839 TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGC 898
Db        261 AGGGG---AGGAGGCCATAACAATTGTCCAGCACTCTTCACCTCCCGGCCTGATCGTGAC 317

Qy        899 CTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCT 958
Db        318 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCTGTCTCAGTT 377

Qy        959 GCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTG 1018
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Db        378 TTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTCAACAACCCTCCATTGTCCAACCTG 437

Qy       1019 TGTGCAGCCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGC 1078
              |||   | |  | || ||||||| ||||   |  | |   |  |||  ||||  ||  |
Db        438 TGT---GGCTTTGGGGACCTGTTTCAGTGCTCCTTCTC---TTCCCTATCCCAATGGTAC 491

Qy       1079 CACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAG 1138
              ||||  || ||| | ||  |  || |  || | |||||||  |     |      ||
Db        492 AACTCGATGCTATCAAGGAAAACTTGAGATCACTGGAGGTGGCATTGAGTCGTCTGTGGA 551

Qy       1139 CATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGG 1198
                | | |||||    |||      | | ||    || ||       | |  |  | | ||
Db        552 GGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTTAGCAGTAGG 611

Qy       1199 GATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGG 1258
                | | | || | | ||    | |      ||||  |   |   |  |   ||    |
Db        612 ACCCATGTTTGTGAGGGAAGCGTGCCCACATCAGCTGCTCACTCAACCTCGAAAGACTGA 671

Qy       1259 TGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCT 1318
                |  |     |       |  |  ||    ||| |   | |  ||||  |||  |||
Db        672 AAATGGGGCCACCTGTCTTCCCATTCCTGTTTGGGGGTTACAGCTACTGCTGCCATTGCT 731

Qy       1319 GTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATT 1356
              |  |     | |  ||  |  |||||   ||  |  ||
Db        732 GCTGCCATCATTTATTCACTTTTCCTAAGAAGGCACTT 769


RESULT 14
US-11-266-748A-342738/c
; Sequence 342738, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 342738
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-342738

  Query Match             4.6%;  Score 73.2;  DB 8;  Length 1000;
  Best Local Similarity   48.0%;  Pred. No. 5e-10;
  Matches  306;  Conservative    0;  Mismatches  323;  Indels    9;  Gaps    3;

Qy        719 TGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCT 778
              | | |||||||||  | |    ||||  || ||     |||    | || ||||| ||  |
Db        860 TAACTGGACCACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 801

Qy        779 GCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT 838
              ||  | ||  | | |||        || || |  |||  || || ||||||| | | |
Db        800 ACTAATAATTAAAGCAGGGACTGAGACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGA 741

Qy        839 TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGC 898
              ||||   |  |  ||   |  |    |  |||||  | ||||| ||  || | ||| |
Db        740 AGGGG---AGGAGGCCATAACAATTGTCCAGCACTCTTCACCTCCCGGCCTGATCGTGAC 684

Qy        899 CTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCT 958
              ||||||  |   ||| |||          | | || |||          ||||         |
Db        683 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCTGTCTCAGTT 624

Qy        959 GCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTG 1018
              | | | |    |  ||||  || ||||  ||  |  ||  || ||||| |||||
Db        623 TTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTCAACAACCCTCCATTGTCCAACCTG 564

Qy       1019 TGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGC 1078
              |||   | |  | || ||||||| ||||   |  | |   |  ||| ||||  ||  |
Db        563 TGT---GGCTTTGGGGACCTGTTTCAGTGCTCCTTCTC---TTCCCTATCCCAATGGTAC 510

Qy       1079 CACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAG 1138
              ||||  || ||| | ||  |  || |  || | |||||||  |     |      ||
Db        509 AACTCGATGCTATCAAGGAAAACTTGAGATCACTGGAGGTGGCATTGAGTCGTCTGTGGA 450

Qy       1139 CATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGG 1198
                | | |||||    |||      | | ||    || ||       | |  |  | | ||
Db        449 GGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTTAGCAGTAGG 390

Qy       1199 GATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGG 1258
                | | | || | | ||    | |      ||||  |   |   |  |   ||    |
Db        389 ACCCATGTTTGTGAGGGAAGCGTGCCCACATCAGCTGCTCACTCAACCTCGAAAGACTGA 330

Qy       1259 TGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCT 1318
                |  |     |       |  |  ||    ||| |   | |  ||||  |||  |||
Db        329 AAATGGGGCCACCTGTCTTCCCATTCCTGTTTGGGGGTTACAGCTACTGCTGCCATTGCT 270

Qy       1319 GTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATT 1356
              |  |     | |  ||  |  |||||   ||  |  ||
Db        269 GCTGCCATCATTTATTCACTTTTCCTAAGAAGGCACTT 232


RESULT 15
US-11-266-748A-368007/c
; Sequence 368007, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 368007
;   LENGTH: 1092
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;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-368007

  Query Match             4.5%;  Score 72.4;  DB 8;  Length 1092;
  Best Local Similarity   50.8%;  Pred. No. 8.7e-10;
  Matches  253;  Conservative    0;  Mismatches  236;  Indels    9;  Gaps    3;

Qy        719 TGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCT 778
              | | |||||||||  | |    ||||  || ||     |||    | || ||||| ||  |
Db        762 TAACTGGACCACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 703

Qy        779 GCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT 838
              ||  | ||  | | |||         || || |  |||  || || ||||||| | | |
Db        702 ACTAATAATTAAAGCAGGGACTGAGACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGA 643

Qy        839 TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGC 898
              ||||   |  | ||   |  |     |   ||||| | ||||| ||  || | ||| |
Db        642 AGGGG---AGGAGGCCATAACAATTGTCCAGCACTCTTCACCTCCCGGCCTGATCGTGAC 586

Qy        899 CTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCT 958
              |||||| |   ||| |||         | | || |||        ||||        |
Db        585 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCTGTCTCAGTT 526

Qy        959 GCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTG 1018
                | | |        |   |||| || ||||  ||  |  ||  || ||||| |||||
Db        525 TTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTCAACAACCCTCCATTGTCCAACCTG 466

Qy       1019 TGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGC 1078
              |||   | |  | || |||||||  ||||   | ||     |  |||| ||||  ||  |
Db        465 TGT---GGCTTTGGGGACCTGTTTCAGTG---CTCCTTCTCTTCCCTGTCCCAATGGTAC 412

Qy       1079 CACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAG 1138
              ||||  || ||| | ||  |  || |  || | |||||||  |      |    ||
Db        411 AACTCGATGCTATCAAGGAAAACTTGAGATCACTGGAGGTGGCATTGAGTCGTCTGTGGA 352

Qy       1139 CATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGG 1198
                |  | |||||    |||       |  | ||    || ||       | |  |  | | ||
Db        351 GGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTTAGCAGTAGG 292

Qy       1199 GATCTTCTCTGCGCGTGA 1216
                | |   || | | ||
Db        291 ACCCATGGTTGTGAGGGA 274


Search completed: July 11, 2006, 10:55:58
Job time : 454 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 10:47:38 ; Search time 2118 Seconds
(without alignments)
9282.444 Million cell updates/sec

Title: US-10-727-619-1
Perfect score: 1600
Sequence: 1 aaaagcagaaagagattacc.....ctgataatacagaccctgtc 1600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1600	100.0	1600	9	US-10-727-619-1	Sequence 1, Appli
2	1599.6	100.0	1630	9	US-10-723-860-3881	Sequence 3881, Ap
3	1598.4	99.9	1692	9	US-10-723-860-7799	Sequence 7799, Ap
4	1579.4	98.7	1587	3	US-09-989-722-354	Sequence 354, App
5	1579.4	98.7	1587	3	US-09-989-723-354	Sequence 354, App
6	1579.4	98.7	1587	3	US-09-989-279-354	Sequence 354, App
7	1579.4	98.7	1587	3	US-09-989-727-354	Sequence 354, App
8	1579.4	98.7	1587	3	US-09-989-731-354	Sequence 354, App
9	1579.4	98.7	1587	3	US-09-989-732-354	Sequence 354, App
10	1579.4	98.7	1587	3	US-09-991-073-354	Sequence 354, App
11	1579.4	98.7	1587	3	US-09-990-442-354	Sequence 354, App
12	1579.4	98.7	1587	3	US-09-991-163-354	Sequence 354, App
13	1579.4	98.7	1587	3	US-09-993-604-354	Sequence 354, App
14	1579.4	98.7	1587	3	US-09-990-456-354	Sequence 354, App
15	1579.4	98.7	1587	3	US-09-989-721-354	Sequence 354, App
16	1579.4	98.7	1587	3	US-09-992-598-354	Sequence 354, App
17	1579.4	98.7	1587	3	US-09-989-293A-354	Sequence 354, App
18	1579.4	98.7	1587	3	US-09-989-735-354	Sequence 354, App
19	1579.4	98.7	1587	3	US-09-990-444-354	Sequence 354, App
20	1579.4	98.7	1587	3	US-09-991-181-354	Sequence 354, App
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33	1579.4	98.7	1587	3	US-09-990-562-354	Sequence 354, App
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40	1579.4	98.7	1587	3	US-09-997-573-354	Sequence 354, App
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42	1579.4	98.7	1587	3	US-09-990-726-354	Sequence 354, App
43	1579.4	98.7	1587	3	US-09-997-559-354	Sequence 354, App
44	1579.4	98.7	1587	3	US-09-997-601-354	Sequence 354, App
45	1579.4	98.7	1587	3	US-09-990-443-354	Sequence 354, App

ALIGNMENTS

RESULT 1
US-10-727-619-1
; Sequence 1, Application US/10727619
; Publication No. US20040259110A1
; GENERAL INFORMATION:
; APPLICANT: PAHL, HEIKE
; TITLE OF INVENTION: PRV-1 AND THE USE THEREOF
; FILE REFERENCE: LEDER-1
; CURRENT APPLICATION NUMBER: US/10/727,619
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/830,189
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/EP99/07238
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 198 49 044.5
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-619-1

Query Match 100.0%; Score 1600; DB 9; Length 1600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
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Qy       301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
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Qy       481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
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Qy      1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
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RESULT 2
US-10-723-860-3881
; Sequence 3881, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3881
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-3881

Query Match 100.0%; Score 1600; DB 9; Length 1630;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1599; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db       1561 GGAGGARTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600


RESULT 3
US-10-723-860-7799
; Sequence 7799, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7799
;   LENGTH: 1692
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-860-7799

  Query Match             99.9%;  Score 1598.4;  DB 9;  Length 1692;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy       481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
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Db       481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy       541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
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Db       541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy       601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Qy       661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
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Db       661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy       721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
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Qy       781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
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Qy       841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900
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Qy       901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
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Db       901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Qy       961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
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Db       961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy      1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy      1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
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Db      1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy      1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
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Db      1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy      1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
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Db      1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy      1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
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Db      1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy      1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
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Db      1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy      1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
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Db      1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy      1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
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Db      1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy      1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
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Db      1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy      1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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Db      1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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RESULT 4
US-09-989-722-354
; Sequence 354, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Qy 80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
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Db 61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

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Qy       140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
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Db       121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy       200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy       260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
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Db       241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy       320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
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Db       361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy       440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Db       421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy       500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
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Db       481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy       560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Db       541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy       620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Db       601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy       680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
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Db       661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy       740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Qy       800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
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Db       781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

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Db       841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy       920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
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Db       901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

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Db      1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy      1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Db      1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy      1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
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Db      1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy      1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
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Db      1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy      1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
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Db      1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy      1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy      1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
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Db      1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy      1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
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Db      1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy      1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
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Db      1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy      1580 TCTGATAATACAGACCCTGTC 1600
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Db      1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 5
US-09-989-723-354
; Sequence 354, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
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;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
```

; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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RESULT 7
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; Sequence 354, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1580 TCTGATAATACAGACCCTGTC 1600
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RESULT 8
US-09-989-731-354
; Sequence 354, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C70
;  CURRENT APPLICATION NUMBER: US/09/989,731
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
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;  PRIOR APPLICATION NUMBER: 60/075945
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
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Qy     200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
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Db     181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

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Qy     380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
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Db     361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy     440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Db     421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy     500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
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Db     481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy     560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Db     541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

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Db     601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy     680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
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Qy     800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
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Db     781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

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Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
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RESULT 9
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; Sequence 354, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
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;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
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;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Patent No. US20020127576A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C15
;  CURRENT APPLICATION NUMBER: US/09/991,073
;  CURRENT FILING DATE:  2001-11-14
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;  PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Qy       1040 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
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Db       1021 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
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Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
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Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
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Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
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Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
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Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
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Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
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Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 11
US-09-990-442-354
; Sequence 354, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             98.7%;  Score 1579.4;  DB 3;  Length 1587;
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Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
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Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

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Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
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Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

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Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

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Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
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Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

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Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

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Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
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Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
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Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

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Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
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Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
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Qy       1580 TCTGATAATACAGACCCTGTC 1600
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RESULT 12
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; Sequence 354, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;  PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
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; APPLICANT: Napier,Mary A.
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
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;  PRIOR FILING DATE: 1998-07-09

  Query Match             98.7%;  Score 1579.4;  DB 3;  Length 1587;
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Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

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Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
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Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

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Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

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Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

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Qy       1580 TCTGATAATACAGACCCTGTC 1600
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; Sequence 354, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C22
;  CURRENT APPLICATION NUMBER: US/09/990,456
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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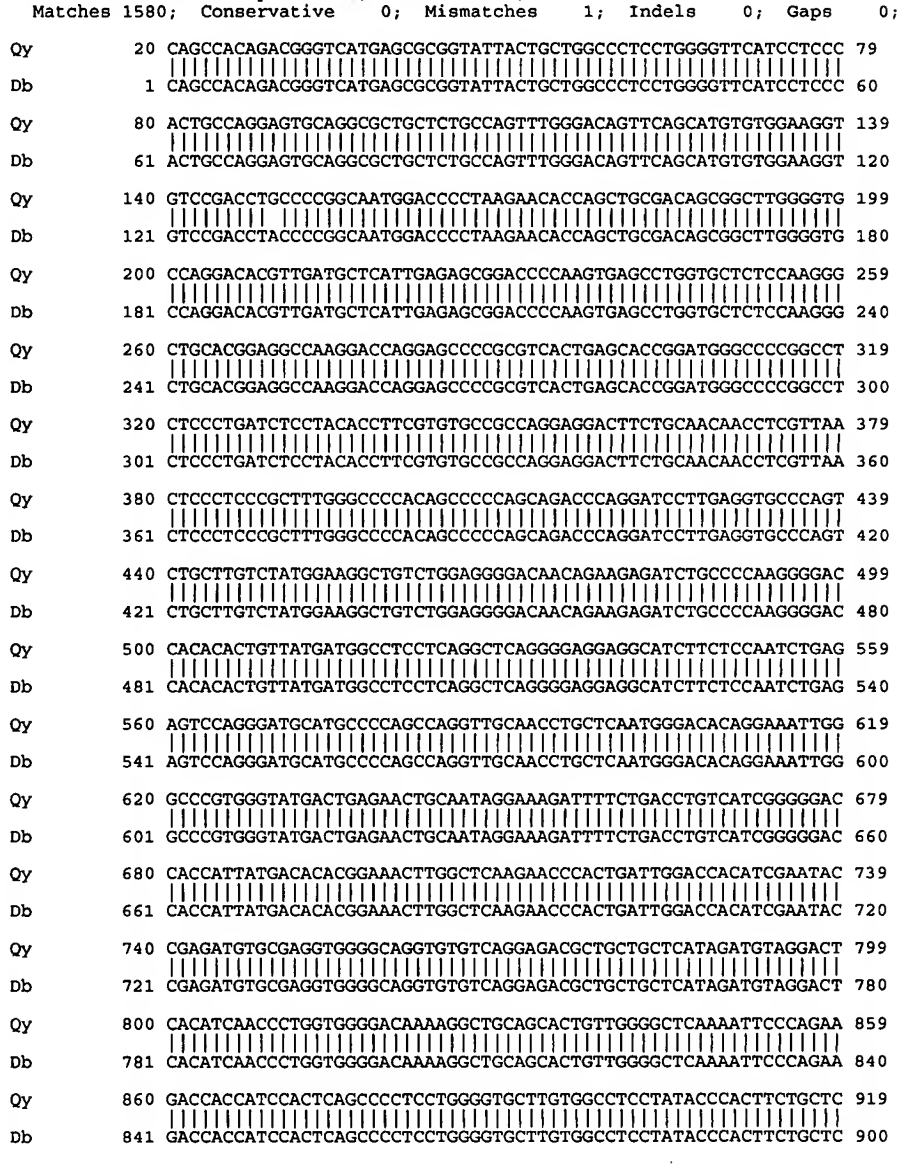

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Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
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RESULT 15
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; Sequence 354, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C55
;  CURRENT APPLICATION NUMBER: US/09/989,721
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
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Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
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Qy       560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Qy       620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Qy       680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
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Qy       860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
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Qy       920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
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Qy       980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
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Db       961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy      1040 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
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Db      1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy      1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Qy      1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
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Qy      1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
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Qy      1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
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Search completed: July 11, 2006, 11:23:08
Job time : 2122 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 10:35:02 ; Search time 7954 Seconds
(without alignments)
11248.545 Million cell updates/sec

Title: US-10-727-619-1
Perfect score: 1600
Sequence: 1 aaaagcagaaagagattacc.....ctgataatacagaccctgtc 1600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1565.6	97.8	2146	6	CR592446	CR592446 full-leng
2	1540.6	96.3	1555	6	CR608112	CR608112 full-leng
3	991	61.9	1048	1	AL545603	AL545603 AL545603
4	928.8	58.1	986	5	CD514938	CD514938 AGENCOURT
c 5	898.2	56.1	1043	1	AL543219	AL543219 AL543219
6	840.8	52.5	901	3	BQ894891	BQ894891 AGENCOURT
7	825.4	51.6	827	8	CX167363	CX167363 HESC2_51_
c 8	816	51.0	883	4	BX371592	BX371592 BX371592
9	809.4	50.6	923	1	AL543254	AL543254 AL543254
10	754.4	47.1	894	2	BI758869	BI758869 603042311
c 11	736	46.0	883	4	BX371593	BX371593 BX371593
12	705.4	44.1	729	4	BX644504	BX644504 DKFZp781B
13	695.8	43.5	766	9	DA728784	DA728784 DA728784
14	660.6	41.3	727	5	CD630132	CD630132 56054680J
15	621.8	38.9	627	8	CV029587	CV029587 8426 Full
16	602.8	37.7	648	3	BP265070	BP265070 BP265070
17	581.4	36.3	583	9	DA762759	DA762759 DA762759
18	580.4	36.3	582	3	BP262687	BP262687 BP262687
19	579	36.2	579	9	DA877430	DA877430 DA877430
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22	577.4	36.1	579	9	DA879021	DA879021 DA879021
23	576.8	36.0	580	9	DA879827	DA879827 DA879827
24	576	36.0	577	9	DA465254	DA465254 DA465254
25	575.4	36.0	577	9	DA429110	DA429110 DA429110
26	575	35.9	575	9	DA874844	DA874844 DA874844
27	574.8	35.9	578	9	DA430711	DA430711 DA430711
28	574.4	35.9	576	9	DA425975	DA425975 DA425975
29	574	35.9	575	9	DA878947	DA878947 DA878947
30	572.8	35.8	576	9	DA432016	DA432016 DA432016
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32	571.8	35.7	575	9	DA429649	DA429649 DA429649
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35	569.4	35.6	571	9	DA428010	DA428010 DA428010
36	569.4	35.6	572	9	DA425980	DA425980 DA425980
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38	569	35.6	569	9	DA865755	DA865755 DA865755
39	569	35.6	569	9	DA876453	DA876453 DA876453
40	568.4	35.5	570	9	DA427412	DA427412 DA427412
41	568.4	35.5	570	9	DA430759	DA430759 DA430759
42	568.4	35.5	571	1	AU310872	AU310872 AU310872
43	567.6	35.5	574	3	BP221450	BP221450 BP221450
44	567.4	35.5	569	9	DA428316	DA428316 DA428316
45	566.8	35.4	570	9	DA878296	DA878296 DA878296

ALIGNMENTS

RESULT 1
CR592446
LOCUS CR592446 2146 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI015YO17 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR592446
VERSION CR592446.1 GI:50473253
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2146)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 2146)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .2146
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI015YO17"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN

Query Match 97.8%; Score 1565.6; DB 6; Length 2146;

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  Matches 1571;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         21 AGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCA 80
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Db          1 AGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCA 60

Qy         81 CTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTG 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        141 TCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGC 200
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Qy        201 CAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGC 260
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Qy        261 TGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTC 320
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Qy        321 TCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAAC 380
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Qy        381 TCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTC 440
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Qy        441 TGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACC 500
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Qy        501 ACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGA 560
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Qy        561 GTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGG 620
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Db        541 GTCCAGGGATGCATGCCCCAGCCAGTTTGCAACCTGCTCAATGGGACACAGGAAATTGGG 600

Qy        621 CCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACC 680
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Qy        681 ACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACC 740
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Db        661 ACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACC 720

Qy        741 GAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTC 800
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Db        721 GAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCCTAGATGTAGGACTC 780

Qy        801 ACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAG 860
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Qy        861 ACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTCC 920
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Qy        981 GCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGT 1040
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Qy       1041 TCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTAC 1100
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Qy       1161 CCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAG 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAG 1200

Qy       1221 CGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCT 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCT 1260

Qy       1281 CTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCT 1340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCT 1320

Qy       1341 TCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCT 1400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCT 1380

Qy       1401 CCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGA 1460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGA 1440

Qy       1461 ATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAG 1520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAG 1500

Qy       1521 CCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTAT 1580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTAT 1560

Qy       1581 CTGATAATACAGACCCTGTC 1600
              ||||||||||||||||||||
Db       1561 CTGATAATACAGACCCTGTC 1580
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```
RESULT 2
CR608112
LOCUS       CR608112               1555 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI001YG18 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR608112
VERSION     CR608112.1  GI:50488919
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1555)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1555)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1555
                     /organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI001YG18"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 96.3%; Score 1540.6; DB 6; Length 1555;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy         38 GAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGC 97
Db          1 GAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGC 60

Qy         98 GCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCA 157
Db         61 GCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCA 120

Qy        158 ATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCT 217
Db        121 ATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCT 180

Qy        218 CATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGA 277
Db        181 CATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGA 240

Qy        278 CCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACAC 337
Db        241 CCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACAC 300

Qy        338 CTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC 397
Db        301 CTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC 360

Qy        398 CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGG 457
Db        361 CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGG 420

Qy        458 CTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGG 517
Db        421 CTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGG 480

Qy        518 CCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC 577
Db        481 CCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC 540

Qy        578 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGA 637
Db        541 CCAGCCAGTTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGA 600

Qy        638 GAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGG 697
Db        601 GAACTGCGATATGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGG 660

Qy        698 AAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGG 757
Db        661 AAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGG 720

Qy        758 GCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGG 817
Db        721 GCAGGTGTGTCAGGAGACGCTGCTGCTCCTAGATGTAGGACTCACATCAACCCTGGTGGC 780

Qy        818 GACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGC 877
Db        781 GACCTAAAGCTGCAGCGCTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGC 840

Qy        878 CCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAG 937
Db        841 CCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAG 900

Qy        938 TGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGG 997
Db        901 TGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGG 960

Qy        998 AGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCG 1057
Db        961 AGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCG 1020

Qy       1058 AATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGG 1117
Db       1021 AATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGG 1080

Qy       1118 TGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTT 1177
Db       1081 TGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTT 1140

Qy       1178 GAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCC 1237
Db       1141 GAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCC 1200

Qy       1238 TGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGG 1297
Db       1201 TGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGG 1260

Qy       1298 GCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTA 1357
Db       1261 GCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTA 1320

Qy       1358 CCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAAC 1417
Db       1321 CCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAAC 1380

Qy       1418 CTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACA 1477
Db       1381 CTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACA 1440

Qy       1478 CAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACT 1537
Db       1441 CAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACT 1500

Qy       1538 TGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAG 1592
Db       1501 TGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAG 1555
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RESULT 3
AL545603
LOCUS AL545603 1048 bp mRNA linear EST 25-MAR-2004
DEFINITION AL545603 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI015YO17 5-PRIME, mRNA sequence.
ACCESSION AL545603
VERSION AL545603.3 GI:45746083
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1048)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31267438.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9230.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI015AH09QP1&c=9230.r.

```
FEATURES             Location/Qualifiers
     source          1. .1048
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI015YO17"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             61.9%;  Score 991;  DB 1;  Length 1048;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-249;
  Matches 1025;  Conservative    0;  Mismatches   20;  Indels    2;  Gaps    2;

Qy          21 AGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCA 80
               ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db           1 AGCCACAGACGGGTCATGAGCCCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCA 60

Qy          81 CTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTG 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTG 120

Qy         141 TCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGC 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGC 180

Qy         201 CAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGC 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGC 240

Qy         261 TGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTC 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTC 300

Qy         321 TCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAAC 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAAC 360

Qy         381 TCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTC 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTC 420

Qy         441 TGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACC 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACC 480

Qy         501 ACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGA 560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGA 540

Qy         561 GTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGG 620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGG 600

Qy         621 CCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACC 680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACC 660

Qy         681 ACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACC 740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 ACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACC 720

Qy         741 GAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTC 800
               ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db         721 GAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCCTAGATGTAGGACTC 780

Qy         801 ACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTT-GGGGCTCAAAATTCCCAGAA 859
               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db         781 ACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGGCTCAAAATTCCCAGAA 840

Qy         860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy         920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy         980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
               ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGT-CTACCTGTGTGCAGCCCCTTGGAACTGT 1019

Qy        1040 TTCAAGTGGCTCCCCCCGAATGACCTG 1066
               | |  | | || || || || | |
Db        1020 TCAGTGGCTCCCCGAATGACTGCCCAG 1046


RESULT 4
CD514938
LOCUS       CD514938                986 bp    mRNA    linear   EST 06-JUN-2003
DEFINITION  AGENCOURT_14368747 NIH_MGC_181 Homo sapiens cDNA clone
            IMAGE:30408929 5', mRNA sequence.
ACCESSION   CD514938
VERSION     CD514938.1  GI:31446656
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM492  row: k  column: 18
            High quality sequence stop: 710.
FEATURES             Location/Qualifiers
     source          1. .986
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30408929"
                     /tissue_type="White Matter"
                     /dev_stage="Unknown"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_181"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV
                     (destroyed); Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.42 kb. Library was constructed by
                     (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             58.1%;  Score 928.8;  DB 5;  Length 986;
  Best Local Similarity   96.9%;  Pred. No. 1.4e-232;
  Matches  956;  Conservative    0;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          32 GGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGT 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGT 60
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Qy         92 GCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCC 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCC 120

Qy        152 CCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTT 180

Qy        212 GATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC 240

Qy        272 CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTC 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTC 300

Qy        332 CTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT 360

Qy        392 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTAT 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTAT 420

Qy        452 GGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTA 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTA 480

Qy        512 TGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATG 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATG 540

Qy        572 CATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTAT 631
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATGCCCCAGCCAGTTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTAT 600

Qy        632 GACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGAC 691
              ||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||
Db        601 GACTGAGAACTGCGATATGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGAC 660

Qy        692 ACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGA 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGA 720

Qy        752 GGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCT 780

Qy        812 GGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCA 871
              |||||||   |||||||||||||||||||||||||| | |||||||   |     ||
Db        781 GGTGGGGGACAAAGGCTGCAGCACTGTTGGGGCTCAAATTNCCCAGAAAGACNNACATCA 840

Qy        872 CTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTG 931
              ||||||||||||||||||||||    | ||||||||||||||||||||||||||||||||
Db        841 CTCAGCCCCTCCTGGGGTGCTTTGTGGCTCCTATACCCACTTCTGCTCCTCGGACCTGTG 900

Qy        932 CAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGT 991
              |||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||
Db        901 CAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCT-CTCCAGCTGCCCCTGT 959

Qy        992 CCCAGGAGACCGGCAGTGTCCTACCTG 1018
              ||||||||| |      |||||||||
Db        960 CCCAGGAGACGGCAGTGTTCCTACCTG 986


RESULT 5
AL543219/c
LOCUS       AL543219               1043 bp    mRNA    linear   EST 24-MAR-2004
DEFINITION  AL543219 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI001YG18 3-PRIME, mRNA sequence.
ACCESSION   AL543219
VERSION     AL543219.3  GI:45718783
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1043)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31265066.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            9230.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DI001BD09NP1&c=9230.r.
FEATURES             Location/Qualifiers
     source          1. .1043
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI001YG18"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             56.1%;  Score 898.2;  DB 1;  Length 1043;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-224;
  Matches  923;  Conservative    4;  Mismatches   14;  Indels    2;  Gaps    2;

Qy        650 GAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCA 709
              |||||||||||||||||||||| |||||||||||||||||||||||| |||| |||||
Db        941 GAAAGATTTTCTGACCTGTCATC-GGGGACCACCATTATGACACACGGACACTTTGCTCA 883

Qy        710 AGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 AGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 823

Qy        770 GGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTG 829
              |||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||||
Db        822 GGAGACGCTGCTGCTCCTAGATGTAGAACTCACATCAACCCTGGTGGGGACAAAAGGCTG 763

Qy        830 CAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGT 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 CAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGT 703

Qy        890 GCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 GCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG 643

Qy        950 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTG 1009
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        642 CAGCGTTCTGCTGTACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTG 583

Qy       1010 TCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCC 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 TCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCC 523

Qy       1070 CAGGGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCAC 1129
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 CAGGGGCACCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCAC 463
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Qy       1130 CAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAG 1189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 CAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAG 403

Qy       1190 ACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCA 1249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCA 343

Qy       1250 TGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGC 1309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 TGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGC 283

Qy       1310 CCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTC 1369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 CCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTC 223

Qy       1370 TTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTG 1429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 TTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTG 163

Qy       1430 GACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATA 1489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 GACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATA 103

Qy       1490 TCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGA 1549
             |||||||||||| |||||||||||||||||||||||||||| |||:|||||||||||||||
Db        102 TCTACTCACCTNACAGCAACACTGGGGAGAGCCTGGAGCAGCCGKACTTGCCCTATGGGA 43

Qy       1550 GAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAG 1592
             ||||   |||||||||| | |||||:|||:  |:|||||||||
Db         42 GAGGNNGCGCTGGAGGANT-GCTGCDTGTRNNTKATAATACAG 1

RESULT 6
BQ894891
LOCUS       BQ894891                901 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8616434 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302444
            5', mRNA sequence.
ACCESSION   BQ894891
VERSION     BQ894891.1  GI:22286905
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 901)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2519  row: o  column: 21
            High quality sequence stop: 647.
FEATURES             Location/Qualifiers
     source          1. .901
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6302444"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             52.5%;  Score 840.8;  DB 3;  Length 901;
  Best Local Similarity   98.7%;  Pred. No. 1.9e-209;
  Matches  889;  Conservative    0;  Mismatches    8;  Indels    4;  Gaps    4;

Qy        107 CCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCC 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCC 60

Qy        167 TAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAG 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAG 120

Qy        227 CGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCC 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCC 180

Qy        287 CCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTG 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTG 240

Qy        347 CCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCC 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCC 300

Qy        407 CCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGA 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGA 360

Qy        467 GGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAG 420

Qy        527 GCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG 586
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        421 GCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCTCAGCCAGG 480

Qy        587 TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAA 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAA 540

Qy        647 TAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGC 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGC 600

Qy        707 TCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTG 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTG 660

Qy        767 TCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGG 826
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        661 TCAGGAGACGCTGCTGCTCCTAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGG 720

Qy        827 CTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAG-CCCCTCCTG 885
              |||||||||||||||||| |||||||||||||||||||||||||||||| |||||||||
Db        721 CTGCAGCACTGTTGGGGCTCANAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTG 780

Qy        886 GGGTGC-TTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCA-G 943
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 GGGTGCTTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGG 840

Qy        944 CAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCG 1003
              |||||||||||||||||||||||||  ||  ||| |||||||||||||||| ||||||
Db        841 CAGCAGCAGCGTTCTGCTGAACTCCCCTCCCTCTC-AGCTGCCCCCTGTCCCAGAAGACCG 899

Qy       1004 G 1004
              |
Db        900 G 900
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RESULT 7
CX167363
LOCUS       CX167363                827 bp    mRNA    linear   EST 23-DEC-2004
DEFINITION  HESC2_51_P11.g1_A035 NIH_MGC_258 Homo sapiens cDNA clone
            IMAGE:7471271 5', mRNA sequence.
ACCESSION   CX167363
VERSION     CX167363.1  GI:56797443
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 827)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: BresaGen, Inc.
             cDNA Library Preparation: Express Genomics, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
            University of Georgia
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15774  row: l  column: 21
            Seq primer: JENREV (CAGGAAACAGCTATGACC)
            High quality sequence stop: 827.
FEATURES             Location/Qualifiers
     source          1. .827
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7471271"
                     /sex="male"
                     /tissue_type="human embryonic stem cells differentiated to
                     an early endodermal cell type"
                     /cell_type="human embryonic stem cells"
                     /cell_line="BG01"
                     /lab_host="DH10B-T1 phage-resistant E. coli"
                     /clone_lib="NIH_MGC_258"
                     /note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
                     RNA obtained from human embryonic stem cells isolated from
                     the inner cell mass of blastocyst stage embryos and
                     differentiated to an early endodermal cell type. Cell line
                     id and NIH Registry designation is BG01. Positive for
                     GATA4, MixL1, Msx1, HNF4alpha expression; negative for AFP
                     expression. Passage number 40. cDNA primed using oligo-dT
                     primer: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and
                     cloned into the EcoRV/NotI sites of pExpress-1. This
                     primary library is non-normalized (normalized primary
                     library is NIH_MGC_259). It was constructed by Express
                     Genomics (Frederick, MD). Sequence ends have been trimmed
                     to exclude vector and regions below Phred quality 16.
                     Three-prime sequences are presented as their reverse
                     complement and have been trimmed to exclude polyA. Note:
                     this is a Mammalian Gene Collection library."
ORIGIN

  Query Match             51.6%;  Score 825.4;  DB 8;  Length 827;
  Best Local Similarity   99.9%;  Pred. No. 2.1e-205;
  Matches  826;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCCTAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTC 846
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTC 827


RESULT 8
BX371592/c
LOCUS       BX371592                883 bp    mRNA    linear   EST 27-APR-2004
DEFINITION  BX371592 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI015YO17 3-PRIME, mRNA sequence.
ACCESSION   BX371592
VERSION     BX371592.2  GI:46625729
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 8, 2003 this sequence version replaced gi:30456041.
            Contact: Genoscope
```

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            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            9230.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAI018ZF05_CS01670_1&c=9230.r
            .
FEATURES             Location/Qualifiers
     source          1. .883
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI015YO17"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             51.0%;  Score 816;  DB 4;  Length 883;
  Best Local Similarity   96.6%;  Pred. No. 6.3e-203;
  Matches  854;  Conservative    0;  Mismatches   27;  Indels    3;  Gaps    2;

Qy        415 ACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAA 474
              ||||||  |||||||||||| |||||||||||| |  ||| ||| |||||||  |||| ||||
Db        883 ACCCAGAATCCTTGAGGT-CCCAGTCTGCTTTTTAATGAAAGNCTGTCTGAAGGGAACAA 825

Qy        475 CAGAAGAGATCTGCCCC--AAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAG 532
              || || ||       |||  ||||||||||||||||||||||||||| ||||||||||
Db        824 CAAAAAAGGATCTGCCCCAAAGGGGACCACACACTGTTATGATGGCCTCTTCAGGCTCAG 765

Qy        533 GGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAA 592
              || |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||||
Db        764 GGAAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGAATGCATGCNCCAGCCAGGTTGCAA 705

Qy        593 CCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAA 652
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        704 CCTGCTCAATGGACAACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAA 645

Qy        653 AGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGA 712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 AGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGA 585

Qy        713 ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGA 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGA 525

Qy        773 GACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAG 832
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        524 GACGCTGCTGCTCCTAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAG 465

Qy        833 CACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCT 892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 CACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCT 405

Qy        893 TGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAG 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAG 345

Qy        953 CGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 CGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCC 285

Qy       1013 TACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAG 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 TACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAG 225

Qy       1073 GGGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAA 1132
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GGGCACCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAA 165

Qy       1133 AATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACA 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 AATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACA 105

Qy       1193 AATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 AATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGA 45

Qy       1253 GGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGG 1296
              |||||||||||||||||||||||||||||||||||||||||||  ||
Db         44 GGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGG 1


RESULT 9
AL543254
LOCUS       AL543254                923 bp    mRNA    linear   EST 24-MAR-2004
DEFINITION  AL543254 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI001YG18 5-PRIME, mRNA sequence.
ACCESSION   AL543254
VERSION     AL543254.3  GI:45718817
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 923)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31265101.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            9230.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DI001BD09QP1&c=9230.r.
FEATURES             Location/Qualifiers
     source          1. .923
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI001YG18"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             50.6%;  Score 809.4;  DB 1;  Length 923;
  Best Local Similarity   98.4%;  Pred. No. 3.4e-201;
  Matches  847;  Conservative    2;  Mismatches    8;  Indels    4;  Gaps    3;

Qy         38 GAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGC 97
              || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GATCCCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGC 60

Qy         98 GCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCA 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCA 120
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Qy        158 ATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCT 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCT 180

Qy        218 CATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGA 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGA 240

Qy        278 CCAGGAGCCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACAC 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCAGGAGCCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACAC 300

Qy        338 CTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC 360

Qy        398 CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGG 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGG 420

Qy        458 CTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGG 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGG 480

Qy        518 CCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC 540

Qy        578 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGA 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGA 600

Qy        638 GAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGG 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGG 660

Qy        698 AAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGG 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGG 720

Qy        758 GCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGG 817
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        721 GCAGGTGTGTCAGGAGACGCTGCTGCTCCTAGATGTAGGACTCACATCAACCCTGGTGGG 780

Qy        818 GACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGC 877
              ||||||  |    :|||||||||||||||||||||||||||||| ||:|||||||||||
Db        781 GACAAA--GGCTGCRCACTGTTGGGGCTCAAAATTCCCAGAAGA-CAMCATCCACTCAG- 836

Qy        878 CCCTCCTGGGGTGCTTGTGGC 898
              |||||||||||||||||||||
Db        837 CCCTCCTGGGGTGCTTGTGGC 857


RESULT 10
BI758869
LOCUS       BI758869                894 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603042311F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182826 5',
            mRNA sequence.
ACCESSION   BI758869
VERSION     BI758869.1  GI:15750447
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11456  row: e  column: 03
            High quality sequence stop: 869.
FEATURES             Location/Qualifiers
     source          1. .894
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5182826"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             47.1%;  Score 754.4;  DB 2;  Length 894;
  Best Local Similarity   95.2%;  Pred. No. 9.9e-187;
  Matches  855;  Conservative    0;  Mismatches   31;  Indels   12;  Gaps    7;

Qy         18 ACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTC 77
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 ACCAGCCACAGACGGGTCATGAGCCCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTC 60

Qy         78 CCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAG 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAG 120

Qy        138 GTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGG 180

Qy        198 TGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAG 257
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        181 TGCCAGGACACGTTGATGCTCATTGAGAGCGGA-CCCAAGTGAGCCTGGTGCTCTCCAAG 239

Qy        258 GGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGC 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGC 299

Qy        318 CTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTT 359

Qy        378 AACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCA 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCA 419

Qy        438 GTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGG 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGG 479

Qy        498 ACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTG 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTG 539

Qy        558 AGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATT 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATT 599
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Qy        618 GGGCCCGTGGGTATGACTGAGAACTGCAATAGGA--AAGATTTTCTGACCTGTCATCGGG 675
              ||||||||||||||||||||||||||||||||||  | ||||||||||||||||||||
Db        600 GGGCCCGTGGGTATGACTGAGAACTGCAATAGGAACACGATTTTCTGACCTGTCATCGGG 659

Qy        676 GGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGA 735
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        660 GGACCACCATTATGACACACGGAAAC-TGGCTCAAGAACCCACTGATTGGACCACATCGA 718

Qy        736 ATACCGAGATGTGCGAGGTGGGG-CAGGTGTGTCAGG----AGACGCTGCTGCTCATAGA 790
              |||||||||||||||||||||||| |||||||||||||     |  |||      |
Db        719 ATACCGAGATGTGCGAGGTGGGGCCAGGTGTGTCAGGGAGACGCTGCTTGCTTCCTAGAT 778

Qy        791 TGTAGGACTCACATCAACCCTGGT-GGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAA 849
              ||| |||||||||| |||||||| |||||||| |||||||||||| || ||||    ||
Db        779 TGTTGGACTCACATCGACCCTGGTGGGGGACAACAGGCTGCAGCACGGTAGGGGGCTCAA 838

Qy        850 ATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATAC 907
              | | |||||||||||||||||||||||||    | |||| ||||||||||||||| |
Db        839 AATTCCAGAAGACCACCATCCACTCAGCCC--TCCGGGGGGCTTGTGGCCTCCTATTC 894


RESULT 11
BX371593/c
LOCUS       BX371593                883 bp    mRNA    linear   EST 27-APR-2004
DEFINITION  BX371593 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI015YO17 3-PRIME, mRNA sequence.
ACCESSION   BX371593
VERSION     BX371593.2  GI:46625731
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 8, 2003 this sequence version replaced gi:30456042.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            9230.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAI018ZF05_CS01670_2&c=9230.r
            .
FEATURES             Location/Qualifiers
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                     /clone="CS0DI015YO17"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             46.0%;  Score 736;  DB 4;  Length 883;
  Best Local Similarity   93.5%;  Pred. No. 6.8e-182;
  Matches  812;  Conservative    0;  Mismatches   50;  Indels    6;  Gaps    4;

Qy        430 GGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCC 489
              || ||||  |   |||||| ||| |||      | |||||   | || || || | ||||
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Db        870 GGGGCCCCATTCTCTTGTCAATGAAAGCTGTCTTAGAGGGACAACCAAAAAAGTTTTGCC 811

Qy        490 CC-AAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTC 548
              || ||||||||| ||| |||| || | | |  |   ||| ||||||  ||||||  |||
Db        810 CCAAAGGGGACCCCACCCTGTAATAAGGCCTCCTCAAGGTTCAGGGAGGGAGGCTCCTTT 751

Qy        549 TCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCA--GGTTGCAACCTGCTCAATGGGA 606
              |||||||||||||||||| |||||||||||||||  | |   ||||||||||||||||
Db        750 TCCAATCTGAGAGTCCAGGAATGCATGCCCCAGCCAAGGTTGCAAACCTGCTCAATGGGA 691

Qy        607 CACAGG--AAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGAC 664
              ||||||  || | |||||||||||||||||||||||||||| ||||||||||||||||||
Db        690 CACAGGGAAATTGGGGCCCGTGGGTATGACTGAGAACTGCCATAGGAAAGATTTTCTGAC 631

Qy        665 CTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTG 724
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CTGTCATC-GGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTG 572

Qy        725 GACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCT 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCT 512

Qy        785 CATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGC 844
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CCTAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGC 452

Qy        845 TCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTA 904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 TCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTA 392

Qy        905 TACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA 964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 TACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA 332

Qy        965 CTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCA 1024
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 CTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCA 272

Qy       1025 GCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCA 1084
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        271 GCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCACCACTCA 212

Qy       1085 TTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCA 1144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCA 152

Qy       1145 GGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTT 1204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTT 92

Qy       1205 CTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGC 1264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGC 32

Qy       1265 TGAGGGCCTGGAGTCTCTCACTTGGGGG 1292
              |||||||||||||||||||||||||||||
Db         31 TGAGGGCCTGGAGTCTCTCACTTGGGGG 4


RESULT 12
BX644504
LOCUS       BX644504                729 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp781B2333_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
            DKFZp781B2333 5', mRNA sequence.
ACCESSION   BX644504
VERSION     BX644504.1  GI:34478837
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 729)
```

```
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
            Wellenreuther,R., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp781B2333) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp781B2333"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="781 (synonym: hlcc4)"
                     /note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match             44.1%;  Score 705.4;  DB 4;  Length 729;
  Best Local Similarity   99.2%;  Pred. No. 7.2e-174;
  Matches  709;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          9 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCCCGGTATTACTGCTGGCCC 68

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         69 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGTGACAG 128

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 188

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        189 GCGACAGCGGCTTGGGGTGCCAGGACACGTCGATGCTCATTGAGAGCGGACCCCAAGTGA 248

Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 308

Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 368

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 428

Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 488

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
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Db        489 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 548

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 608

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
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Db        609 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 668

Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACC 715
              |||||||||||||||||||||||||||||||||||||||||||||||||||  | ||
Db        669 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAGAACCC 723


RESULT 13
DA728784
LOCUS       DA728784                 766 bp    mRNA    linear   EST 11-NOV-2005
DEFINITION  DA728784 NT2RM2 Homo sapiens cDNA clone NT2RM2002461 5', mRNA
            sequence.
ACCESSION   DA728784
VERSION     DA728784.1  GI:81802098
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES             Location/Qualifiers
     source          1. .766
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="NT2RM2002461"
                     /cell_type="teratocarcinoma"
                     /cell_line="NT2"
                     /clone_lib="NT2RM2"
                     /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
                     precursor cells"
ORIGIN

  Query Match             43.5%;  Score 695.8;  DB 9;  Length 766;
  Best Local Similarity   98.1%;  Pred. No. 2.4e-171;
  Matches  734;  Conservative    0;  Mismatches   10;  Indels    4;  Gaps    3;

Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 81

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
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Db        82 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 141

Qy       121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
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Db       142 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 201

Qy       181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       202 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 261

Qy       241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
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Db       262 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 321

Qy       301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       322 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 381

Qy       361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       382 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 441

Qy       421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
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Db       442 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 501

Qy       481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       502 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 561

Qy       541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       562 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 621

Qy       601 ATGGGACACAGGAAATTGGG-CCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTT 659
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db       622 ATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGAATTT 681

Qy       660 CTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACT 719
            |||||     |||||||||||||||||||||||||| | ||||||||| ||| ||||  |
Db       682 CTGAC--TGTATCGGGGGACCACCATTATGACACACNGNAACTTGGCTTAAG-ACCCCTT 738

Qy       720 GATTGGACCACATCGAATACCGAGATGT 747
            |||||||||||||||||||||||| ||||
Db       739 GATTGGACCACATCGAATACCGANATGT 766


RESULT 14
CD630132
LOCUS       CD630132                727 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  56054680J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD630132
VERSION     CD630132.1  GI:40278398
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 727)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
   PUBMED   15203218
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .727
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             41.3%;  Score 660.6;  DB 5;  Length 727;
  Best Local Similarity   98.5%;  Pred. No. 4.3e-162;
  Matches  719;  Conservative    0;  Mismatches    5;  Indels    6;  Gaps    5;

Qy        868 TCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACC 927
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Db          1 TCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACC 60

Qy        928 TGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCC 987
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCC 120

Qy        988 CTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTG 1047
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Db        121 CTGTCCCAGGAGACCGGCAGTGTTCTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTG 180

Qy       1048 GCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTACATTCATC 1107
            |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||
Db        181 GCTCCCCCCGAATGACCTGCCCCA-GGGCACCACTCATTGTTATGATGGGTACATTCATC 239

Qy       1108 TCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCA 1167
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCA 299

Qy       1168 GCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATG 1227
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATG 359

Qy       1228 TGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTT 1287
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        360 TGCAGCCTCCTGCCTCTCAGCATGAGAGAGGTGGGGCTGAGGGCCTGGAGTCTCTCACTT 419

Qy       1288 GGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCT 1347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTCCTGCT 479

Qy       1348 AACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTG 1407
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Db        480 AACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTCTG 539

Qy       1408 ACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGAATCATCT 1467
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Db        540 ACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATGAATCATCT 599

Qy       1468 TCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGG--AGAGCCTGG 1525
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Db        600 TCCCCA-ACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGGAAGAGCCTGG 658

Qy       1526 AGCATCCGGAC-TTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGA 1584
            ||||  ||||| ||||||||||||||||||||||||||||||||| ||||||||||||||
Db        659 AGCANGCGGACTTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGG-TGCATGTATCTGA 717

Qy       1585 TAATACAGAC 1594
            ||||||||||
Db        718 TAATACAGAC 727


RESULT 15
CV029587
LOCUS       CV029587                627 bp    mRNA    linear   EST 20-AUG-2004
DEFINITION  8426 Full Length cDNA from the Mammalian Gene Collection Homo
            sapiens cDNA 5' similar to BC029167, mRNA sequence.
ACCESSION   CV029587
VERSION     CV029587.1  GI:51487767
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 627)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
            Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
            Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
            Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
            Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE     Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
            results from a PCR reaction using an MGC full-length cDNA as
            template DNA and ORF specific primers
            PCR PRimers
            FORWARD: ATGAGCCCGGTATTACTG
            BACKWARD: TAGCAGGAAGGGCAAACCA
            Insert Length: 627    Std Error: 53.00
            Plate: 11036  row: 06  column: G
            Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
            High quality sequence start: 96
            High quality sequence stop: 626
            POLYA=No.
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="mixed"
                      /clone_lib="Full Length cDNA from the Mammalian Gene
                      Collection"
                      /note="Vector: mixed; The ORFs were PCR amplified from the
                      MGC (Mammalian Gene Collection) as of April 2004 and
                      cloned by recombinational Gateway cloning into pDONR223
                      Donor vector. Reference : MGC (Mammalian Gene Collection)
                      Program Team, Generation and Initial Analysis of more than
                      15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                      2002, 99(26), 16899-16903"
ORIGIN

  Query Match             38.9%;  Score 621.8;  DB 8;  Length 627;
  Best Local Similarity   99.4%;  Pred. No. 6.6e-152;
  Matches  623;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         36 ATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAG 95
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGCCCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAG 60

Qy         96 GCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGG 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGG 120

Qy        156 CAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATG 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATG 180

Qy        216 CTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAG 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAG 240

Qy        276 GACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTAC 335
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Db        241 GACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTAC 300

Qy        336 ACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGG 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGG 360

Qy        396 GCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAA 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        456 GGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT 515
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GenCore version 5.1.9

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	1579.4	98.7	1587	3	US-09-990-444-354	Sequence 354, App
	4	1579.4	98.7	1587	3	US-10-033-301-15	Sequence 15, Appl
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	6	1579.4	98.7	1587	3	US-09-992-598-354	Sequence 354, App
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09830189C
; Patent No. 6686153
; GENERAL INFORMATION:
; APPLICANT: PAHL, HEIKE
; TITLE OF INVENTION: PRV-1 AND THE USE THEREOF
; FILE REFERENCE: LEDER-1
; CURRENT APPLICATION NUMBER: US/09/830,189C
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/EP99/07238
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 198 49 044.5
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1600
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; ORGANISM: Homo sapiens
US-09-830-189C-1

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Best Local Similarity 100.0%; Pred. No. 0;
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT FILING DATE: 2001-11-16
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; PRIOR FILING DATE: 1998-07-09

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Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
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Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
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Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
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Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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RESULT 3
US-09-990-444-354
; Sequence 354, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444

; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-02-25
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;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             98.7%;  Score 1579.4;  DB 3;  Length 1587;
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Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

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RESULT 4
US-10-033-301-15
; Sequence 15, Application US/10033301
; Patent No. 6930172
; GENERAL INFORMATION:
;  APPLICANT: Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
```

; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Goddard,Audrey
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Roy,Margaret Ann
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2930R1C6
; CURRENT APPLICATION NUMBER: US/10/033,301
; CURRENT FILING DATE: 2001-12-27
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; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 38
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; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-301-15

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
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RESULT 5
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; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6
US-09-992-598-354
; Sequence 354, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1580 TCTGATAATACAGACCCTGTC 1600
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RESULT 7
US-10-033-435-15
; Sequence 15, Application US/10033435
; Patent No. 6969758
; GENERAL INFORMATION:
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Goddard,Audrey
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Roy,Margaret Ann
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2930R1C5
; CURRENT APPLICATION NUMBER: US/10/033,435
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/095,325
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/112,851
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,145
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,511
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; PRIOR APPLICATION NUMBER: 60/115,558
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; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119,537
; PRIOR FILING DATE: 1999-02-10
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; PRIOR APPLICATION NUMBER: 60/162,506
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; PRIOR APPLICATION NUMBER: 60/170,262
; PRIOR FILING DATE: 1999-12-09
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;  PRIOR FILING DATE: 2000-05-30
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US-10-033-435-15

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Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

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Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
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Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
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Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
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RESULT 8
US-09-989-735-354
; Sequence 354, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
```

; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 4; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

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Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

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Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

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Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
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Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
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Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
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Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581

RESULT 9
US-09-989-726-354
; Sequence 354, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C60
;  CURRENT APPLICATION NUMBER: US/09/989,726
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
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;  APPLICANT:  Roy, Margaret Ann
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;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
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;  TITLE OF INVENTION:  Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 5; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 11
US-09-989-728-354
; Sequence 354, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy,Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C72
;  CURRENT APPLICATION NUMBER: US/09/989,728
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 5; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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RESULT 12
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; Sequence 354, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C37
;  CURRENT APPLICATION NUMBER: US/09/997,349
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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;  PRIOR FILING DATE: 1998-02-25
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;  PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 5; Length 1587;
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Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091626

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;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091633
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091978
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             98.7%;  Score 1579.4;  DB 5;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
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Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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RESULT 14
US-09-989-293A-354
; Sequence 354, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 5; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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RESULT 15
US-09-073-569-1
; Sequence 1, Application US/09073569
; Patent No. 6084088
;  GENERAL INFORMATION:
;    APPLICANT:  Sheppard, Paul O.
;    APPLICANT:  Grossmann, Angelika
;    TITLE OF INVENTION:  NOVEL TUMOR ANTIGENS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/073,569
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sawislak, Deborah A
;      REGISTRATION NUMBER:  37,438
;      REFERENCE/DOCKET NUMBER:  97-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6672
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1733 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  34...1344
;      OTHER INFORMATION:
US-09-073-569-1

  Query Match             98.4%;  Score 1574.6;  DB 3;  Length 1733;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1577;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
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Db        798 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 857

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
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Job time : 327 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1600	100.0	1600	2	AX107816	AX107816 Sequence
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5	1584	99.0	1597	5	HSA290452	AJ290452 Homo sapi
6	1579.4	98.7	1587	2	CQ970596	CQ970596 Sequence
7	1579.4	98.7	1587	2	AR252615	AR252615 Sequence
8	1579.4	98.7	1587	2	AR693505	AR693505 Sequence
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26	1312	82.0	1314	8	AY891246	AY891246 Synthetic
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ALIGNMENTS

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LOCUS BD243146 1600 bp DNA linear PAT 17-JUL-2003
DEFINITION The gene PRV-1 and its use.
ACCESSION BD243146
VERSION BD243146.1 GI:33052916
KEYWORDS JP 2002528077-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1600)
AUTHORS Pahl,H.
TITLE The gene PRV-1 and its use
JOURNAL Patent: JP 2002528077-A 1 03-SEP-2002;
UNIVERSITAETSKLINIKUM FREIBURG
COMMENT OS Homo sapiens (human)
PN JP 2002528077-A/1
PD 03-SEP-2002
PF 30-SEP-1999 JP 2000578440
PR 23-OCT-1998 DE 198 49 044.5
PI HEIKE PAHL
PC C12N15/09,A61K31/7105,A61K31/711,A61K38/00,A61K39/395 PC ,A61K39/395,A61K48/00,
PC A61P7/00,A61P7/02,A61P7/06,A61P9/00,A61P9/12,A61P13/12 PC ,A61P17/04,A61P19/06,
PC A61P25/04,A61P29/00,A61P31/04,A61P35/00,A61P35/02,A61P43/00,
PC C07K14/47,
PC C07K14/475,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/ PC 68,
PC G01N33/53,G01N33/53,G01N33/566,G01N33/577//C12P21/08,C12N15/00, PC C12N5/00,
PC A61K37/02
CC The gene PRV-1 and its use
FH Key Location/Qualifiers
FT source 1. .1600
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FEATURES Location/Qualifiers

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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1600;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
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Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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Db       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600


RESULT 2
AR455749
LOCUS       AR455749               1600 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 1 from patent US 6686153.
ACCESSION   AR455749
VERSION     AR455749.1  GI:42690638
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1600)
  AUTHORS   Pahl,H.
  TITLE     PRV-1 gene and the use thereof
  JOURNAL   Patent: US 6686153-A 1 03-FEB-2004;
            Universitatsklinikum Freiburg; Freiburg;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .1600
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1600;  DB 2;  Length 1600;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1600;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
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Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
Db        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240

Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
Db        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300

Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
Db        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420

Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
Db        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
Db        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
Db        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900
Db        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900

Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
Db        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
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Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
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Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
Db       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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RESULT 3
AX107816
LOCUS       AX107816                1600 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1 from Patent WO0123554.
ACCESSION   AX107816
VERSION     AX107816.1  GI:13923217
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Pahl,H.
  TITLE     The prv-1 gene and use thereof
  JOURNAL   Patent: WO 0123554-A 1 05-APR-2001;
            Universitaetsklinikum Freiburg (DE)
FEATURES             Location/Qualifiers
     source          1. .1600
                     /organism="Homo sapiens"
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ORIGIN

  Query Match             100.0%;  Score 1600;  DB 2;  Length 1600;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1600;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
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Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
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Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
Db        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
Db        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
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Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
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Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
Db        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900
Db        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900
Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
Db        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
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Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
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Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
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Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
Db       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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RESULT 4
AF146747
LOCUS       AF146747               1630 bp    mRNA    linear   PRI 25-OCT-2002
DEFINITION  Homo sapiens cell surface receptor (PRV1) mRNA, complete cds.
ACCESSION   AF146747
VERSION     AF146747.1  GI:9857660
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Temerinac,S., Klippel,S., Strunck,E., Roder,S., Lubbert,M.,
            Lange,W., Azemar,M., Meinhardt,G., Schaefer,H.E. and Pahl,H.L.
  TITLE     Cloning of PRV-1, a novel member of the uPAR receptor superfamily,
            which is overexpressed in polycythemia rubra vera
  JOURNAL   Blood 95 (8), 2569-2576 (2000)
   PUBMED   10753836
REFERENCE   2  (bases 1 to 1630)
  AUTHORS   Temerinac,S., Roeder,S. and Pahl,H.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-1999) Anaesthesiology, University Hospital
            Freiburg, Breisacher Str. 117, Freiburg 79106, Germany
FEATURES             Location/Qualifiers
     source          1. .1630
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                     /db_xref="taxon:9606"
                     /chromosome="19"
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                     /product="cell surface receptor"
                     /protein_id="AAG00895.1"
                     /db_xref="GI:9857661"
                     /translation="MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTP
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                     GLLRLRGGGIFSNLRVQGCMPQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIM
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                     TIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGT
                     CSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSA
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ORIGIN

Query Match 100.0%; Score 1600; DB 5; Length 1630;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1599; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240

Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300

Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420

Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
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Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
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Db        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
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Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900

Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
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Db        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
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Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
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Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
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Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
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Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
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Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
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Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
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Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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Db       1561 GGAGGARTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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RESULT 5
HSA290452

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LOCUS       HSA290452               1597 bp    mRNA    linear   PRI 17-JUL-2001
DEFINITION  Homo sapiens mRNA for NB1 glycoprotein (NB1 gene).
ACCESSION   AJ290452
VERSION     AJ290452.1  GI:14970726
KEYWORDS    NB1 gene; NB1 glycoprotein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kissel,K., Santoso,S., Hofmann,C., Stroncek,D. and Bux,J.
  TITLE     Molecular basis of the neutrophil glycoprotein NB1 (CD177) involved
            in the pathogenesis of immune neutropenias and transfusion
            reactions
  JOURNAL   Eur. J. Immunol. 31 (5), 1301-1309 (2001)
   PUBMED   11465086
REFERENCE   2  (bases 1 to 1597)
  AUTHORS   Kissel,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2000) Kissel K., Justus-Liebig-University,
            Institute for Clinical Immunology and Transfusion Medicine,
            Langhansstrasse 7, 35385 Giessen, GERMANY
FEATURES             Location/Qualifiers
     source          1. .1597
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                     /experiment="experimental evidence, no additional details
                     recorded"
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ORIGIN

  Query Match             99.0%;  Score 1584;  DB 5;  Length 1597;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1587;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 AAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGG 68
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          1 AAAGAGATTACCAGCCACAGACGGGTCATGAGCCCGGTATTACTGCTGGCCCTCCTGGGG 60

Qy         69 TTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCAT 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCAT 120

Qy        129 GTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGC 188
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Db        121 GTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGC 180

Qy        189 GGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTG 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTG 240

Qy        249 CTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATG 308
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Db        241 CTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATG 300

Qy        309 GGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAAC 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAAC 360

Qy        369 AACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTG 428
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Db        361 AACCTCGTTAACTCCCTCCCGTTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTG 420

Qy        429 AGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGC 488
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Db        421 AGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGC 480

Qy        489 CCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTC 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTC 540

Qy        549 TCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACA 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACA 600

Qy        609 CAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGT 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGT 660

Qy        669 CATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACC 728
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Db        661 CATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACC 720

Qy        729 ACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATA 788
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Db        721 ACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATA 780

Qy        789 GATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAA 848
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Db        781 GATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAA 840

Qy        849 AATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACC 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACC 900

Qy        909 CACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCC 968
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Db        901 CACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCC 960

Qy        969 CTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCC 1028
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Db        961 CTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCAGCAGTGTCCTACCTGTGTGCAGCCC 1020

Qy       1029 CTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGT 1088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGT 1080

Qy       1089 TATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGC 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGC 1140

Qy       1149 TGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCT 1208
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1141 TGCGTGGCCCAACCTTCCAGCTCCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCT 1200

Qy       1209 GCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAG 1268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAG 1260

Qy       1269 GGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGA 1328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGA 1320

Qy       1329 GTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACC 1388
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Db       1321 GTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACC 1380

Qy       1389 CACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCA 1448
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Db       1381 CACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCA 1440

Qy       1449 TTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAA 1508
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Qy       1509 CACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGT 1568
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Db       1501 CACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGT 1560
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Qy       1569 GGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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RESULT 6
CQ970596
LOCUS       CQ970596                1587 bp    DNA     linear   PAT 05-JAN-2005
DEFINITION  Sequence 161 from Patent EP1489095.
ACCESSION   CQ970596
VERSION     CQ970596.1  GI:57162779
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Polypeptide, nucleic acid encoding it, and their use for the
            diagnosis of cancer
  JOURNAL   Patent: EP-1489095-A 161 22-DEC-2004;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             98.7%;  Score 1579.4;  DB 2;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
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Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
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Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
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Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
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Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
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Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
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Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
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Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
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Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
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Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
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Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
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Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
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Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
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Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
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Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
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Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
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Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
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Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
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Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581


RESULT 7
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AR252615
LOCUS       AR252615                1587 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 354 from patent US 6478825.
ACCESSION   AR252615
VERSION     AR252615.1  GI:27300523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1587)
  AUTHORS   Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
  TITLE     Implant, method of making same and use of the implant for the
            treatment of bone defects
  JOURNAL   Patent: US 6478825-A 354 12-NOV-2002;
            Osteotech, Inc.; Eatontown, NJ
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             98.7%;  Score 1579.4;  DB 2;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
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Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
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Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
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Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

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RESULT 8
AR693505
LOCUS       AR693505                1587 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 354 from patent US 6913919.
ACCESSION   AR693505
VERSION     AR693505.1  GI:75183962
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1587)
  AUTHORS   Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and
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          Wood,W.I.
  TITLE   Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL Patent: US 6913919-A 354 05-JUL-2005;
          Genetech, Inc.; South San Francisco, CA
FEATURES             Location/Qualifiers
     source          1. .1587
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ORIGIN

  Query Match             98.7%;  Score 1579.4;  DB 2;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
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Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

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Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Db       1561 TCTGATAATACAGACCCTGTC 1581


RESULT 9
AR706057
LOCUS       AR706057               1587 bp    DNA     linear   PAT 20-SEP-2005
DEFINITION  Sequence 354 from patent US 6930170.
ACCESSION   AR706057
VERSION     AR706057.1  GI:75924778
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1587)
  AUTHORS   Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.
  TITLE     PRO1184 polypeptides
  JOURNAL   Patent: US 6930170-A 354 16-AUG-2005;
            Genentech, Inc.; South San Francisco, CA;
            WOX;
FEATURES             Location/Qualifiers
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ORIGIN
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  Query Match             98.7%;  Score 1579.4;  DB 2;  Length 1587;
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  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
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Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
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Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 10
AR706205
LOCUS       AR706205               1587 bp    DNA     linear   PAT 20-SEP-2005
DEFINITION  Sequence 15 from patent US 6930172.
ACCESSION   AR706205
VERSION     AR706205.1  GI:75925073
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1587)
  AUTHORS   Ferrara,N., Gao,W.-Q., Goddard,A., Gurney,A.L., Watanabe,C.K. and
            Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: US 6930172-A 15 16-AUG-2005;
            Genentech, Inc.; South San Francisco, CA
FEATURES             Location/Qualifiers
     source          1. .1587
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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  Query Match             98.7%;  Score 1579.4;  DB 2;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120
Qy       140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
Db       121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180
Qy       200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
Db       181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240
Qy       260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
Db       241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300
Qy       320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
Db       301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360
Qy       380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
Db       361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420
Qy       440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
Db       421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480
Qy       500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
Db       481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540
Qy       560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
Db       541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600
Qy       620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
Db       601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660
Qy       680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
Db       661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720
Qy       740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
Db       721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780
Qy       800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
Db       781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840
Qy       860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
Db       841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900
Qy       920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
Db       901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960
Qy       980 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCCTTGGAACCTG 1039
Db       961 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCCTTGGAACCTG 1020
Qy      1040 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
Db      1021 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080
Qy      1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
Db      1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140
Qy      1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
Db      1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200
Qy      1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
Db      1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260
Qy      1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
Db      1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320
Qy      1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
Db      1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380
Qy      1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
Db      1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440
Qy      1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
Db      1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500
Qy      1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
Db      1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560
Qy      1580 TCTGATAATACAGACCCTGTC 1600
Db      1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 11
AR757430
LOCUS AR757430 1587 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 354 from patent US 6953836.
ACCESSION AR757430
VERSION AR757430.1 GI:83322601
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1587)
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.
TITLE PRO844 polypeptides
JOURNAL Patent: US 6953836-A 354 11-OCT-2005;
Genentech, Inc.; South San Francisco, CA
FEATURES Location/Qualifiers
source 1. .1587
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 98.7%; Score 1579.4; DB 2; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
Db           1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60
Qy          80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
Db          61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120
Qy         140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
Db         121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180
Qy         200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
Db         181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240
Qy         260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
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Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
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Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
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Db        961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
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Db       1021 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
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Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
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Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
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Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
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Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
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Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 12
AR758930

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LOCUS       AR758930               1587 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 354 from patent US 6956108.
ACCESSION   AR758930
VERSION     AR758930.1  GI:83325025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1587)
  AUTHORS   Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.
  TITLE     PRO1184 antibodies
  JOURNAL   Patent: US 6956108-A 354 18-OCT-2005;
            Genentech, Inc.; South San Francisco, CA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .1587
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ORIGIN
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Query Match 98.7%; Score 1579.4; DB 2; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Db           1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy          80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy         140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
               ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy         200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy         260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy         320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy         380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy         440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
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Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581


RESULT 13
AR773790
LOCUS       AR773790               1587 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 15 from patent US 6969758.
ACCESSION   AR773790
VERSION     AR773790.1  GI:83350971
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1587)
  AUTHORS   Ferrara,N., Gao,W.-Q., Goddard,A., Gurney,A.L., Watanabe,C.K. and
            Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: US 6969758-A 15 29-NOV-2005;
            Genentech, Inc.; South San Francisco, CA
FEATURES             Location/Qualifiers
     source          1. .1587
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           98.7%;  Score 1579.4;  DB 2;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
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Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600
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Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
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Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
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Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
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Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
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Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 14
AR776244
LOCUS AR776244 1587 bp DNA linear PAT 08-DEC-2005

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DEFINITION  Sequence 354 from patent US 6972185.
ACCESSION   AR776244
VERSION     AR776244.1  GI:83353584
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1587)
  AUTHORS   Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.
  TITLE     Nucleic acids encoding PRO844 polypeptides
  JOURNAL   Patent: US 6972185-A 354 06-DEC-2005;
            Genentech, Inc.; South San Francisco, CA
FEATURES             Location/Qualifiers
     source          1. .1587
                     /organism="unknown"
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ORIGIN

  Query Match             98.7%;  Score 1579.4;  DB 2;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
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Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
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Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
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Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCCTTGGAACCTG 1039
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Db        961 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
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Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
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Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
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Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
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Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
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Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
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Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
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Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
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Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
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Db       1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 15
AX358908
LOCUS       AX358908               1587 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 161 from Patent WO0193983.
ACCESSION   AX358908
VERSION     AX358908.1  GI:18675355
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0193983-A 161 13-DEC-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1587
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match 98.7%; Score 1579.4; DB 2; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
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Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
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Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
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Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
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Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
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Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
                ||||||||||||||||||||
Db       1561 TCTGATAATACAGACCCTGTC 1581
```

Search completed: July 11, 2006, 14:59:27
Job time : 8849 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:25:06 ; Search time 41 Seconds
(without alignments)
1025.530 Million cell updates/sec

Title: US-10-727-619-2
Perfect score: 2381
Sequence: 1 MSAVLLLALLGFILPLPGVQ.....WGVGLALAPALWWGVVCPSC 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	163	6.8	5376	2	T42215	zonadhesin - mouse
2	143	6.0	1297	2	T30274	proteoliaisin - se
3	142	6.0	330	1	JN0561	urokinase-type pla
4	136.5	5.7	1101	2	T16840	hypothetical prote
5	136.5	5.7	2531	2	A46019	notch-1 protein -
6	131.5	5.5	2813	1	VWHU	von Willebrand fac
7	130	5.5	2946	2	T15840	hypothetical prote
8	128	5.4	1408	2	S16148	gene serrate prote
9	127.5	5.4	1895	2	T15881	hypothetical prote
10	126.5	5.3	2090	2	T30075	hypothetical prote
11	126.5	5.3	2153	2	T30074	hypothetical prote
12	122.5	5.1	677	2	C42125	trophozoite cystei
13	122.5	5.1	1964	2	T09059	notch4 - mouse
14	121.5	5.1	738	2	S40992	hypothetical prote
15	121.5	5.1	739	2	B88553	protein K04H4.2b [
16	121.5	5.1	2318	2	S45306	notch 3 protein -
17	119.5	5.0	327	2	A55356	urokinase-type pla
18	119.5	5.0	1357	2	T16860	hypothetical prote
19	118.5	5.0	1043	2	T19734	hypothetical prote
20	118.5	5.0	3020	2	A43932	mucin 2 precursor,
21	118	5.0	2703	1	A24420	notch protein - fr
22	117.5	4.9	1251	2	A57293	latent transformin
23	117	4.9	2395	1	S50820	surface protein ty
24	117	4.9	3002	2	A47221	fibrillin 1 precur
25	116	4.9	802	2	T24293	hypothetical prote
26	116	4.9	949	2	T24294	hypothetical prote
27	116	4.9	2704	2	S09118	G surface protein
28	115	4.8	667	2	A48579	trophozoite surfac
29	115	4.8	1743	2	T26859	hypothetical prote
30	115	4.8	2555	2	A40043	notch protein homo
31	115	4.8	2871	2	A55567	fibrillin I - bovi
32	115	4.8	2871	2	A55624	fibrillin-1 precur
33	114.5	4.8	1360	2	T33922	hypothetical prote
34	114.5	4.8	2844	2	S28291	hypothetical prote
35	114.5	4.8	3133	2	S52093	hemocytin - silkwo
36	114	4.8	2918	2	A54105	fibrillin-2 precur
37	113.5	4.8	1142	2	T30272	hypothetical prote
38	113.5	4.8	1797	2	T21889	hypothetical prote
39	113.5	4.8	1805	2	T21888	hypothetical prote
40	113.5	4.8	2352	2	T30201	Notch homolog prot
41	113	4.7	2195	2	T34264	hypothetical prote
42	113	4.7	2718	2	A23475	G surface protein
43	112	4.7	385	2	S53718	homeotic protein d
44	112	4.7	589	2	C38128	epithelin/granulin
45	112	4.7	2910	2	T42214	otogelin - mouse

ALIGNMENTS

RESULT 1
T42215
zonadhesin - mouse
N;Alternate names: sperm-specific membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42215
R;Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane p
A;Reference number: Z22080; MUID:98123114; PMID:9452463
A;Accession: T42215
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5376 <GAO>
A;Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:g3327420;
C;Genetics:
A;Gene: Zan
A;Map position: 5
C;Function:
A;Description: functions in multiple cell adhesion processes
A;Note: found exclusively on the apical region of the sperm head
C;Keywords: cell adhesion

Query Match 6.8%; Score 163; DB 2; Length 5376;
Best Local Similarity 20.6%; Pred. No. 0.0028;
Matches 91; Conservative 44; Mismatches 128; Indels 178; Gaps 25;

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Qy         20 QALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGL--GCQDTLMLIESGPQVS---LVLSK 74
              :  :|| | : |             ||  |   :  ||:|     |  :|     :|:
Db       3217 EGCICQPGYLMH------------KN-KCVLRIFCGCKNT-----QGAFISADKTWISR 3257

Qy         75 GCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPADPGS---- 130
              |||::             |  ::    | |    :| |              | ||
Db       3258 GCTQS----------CTCPAGAIHCRNFKCPSGTYCKN------------GDNGSSNCT 3294

Qy        131 ---LRCPVCLSMEGCL-------EGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
                 |:||        ||          |   |   : | :| |     | :||      |:
Db       3295 EITLQCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGCL-CNHGFVFSE---DKCV 3350

Qy        181 PQPGCNLLNGTQEIGPVGMT---ENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTE- 236
              |:  |   :    | | | |   : | :     |  |   :   |    |  :  |:|
Db       3351 PRTQCGCKDARGAIIPAGKTWTSKGCTQS--CACVEGN--IQCQNFQCPPETYCKDNSEG 3406

Qy        237 ---------------------------------------------MCEVGQVCQETLL--- 249
                                                          |: | |||   :
Db       3407 SSTCTKITLQCPAHTQYTSCLPSCLPSCLDPEGLCKDISPKVPSTCKEGCVCQSGYVLNS 3466

Qy        250 ----------------LIDVGLTSTLVG-TKGCSTVG----AQNSQKTTIHSAPPGVLV 287
                           ||  | | |  | |: |: :|     |:||        |||
Db       3467 DKCVLRAECDCKDAQGALIPAGKTWTSPGCTQSCACMGGAVQCQSSQ------CPPGT-- 3518
```

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Qy        288 ASYTHFCSSDLCNSASSSSVLL---------NSLPPQAAPVPGDRQC-PTCVQPLGTCSS 337
                  :|  :   ::: : : |          | |||           | |:|: | | |
Db       3519 -----YCKDNEDGNSNCAKITLQCPAHSLFTNCLPP----------CLPSCLDPDGLCKG 3563

Qy        338 GSPRM--TCPRGATHCYDGYI 356
               ||::  ||  |   |  ||:
Db       3564 ASPKVPSTCKEGCI-CQSGYV 3583


RESULT 2
T30274
proteoliaisin - sea urchin (Strongylocentrotus purpuratus) (fragment)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30274
R;Laidlaw, M.; Wessel, G.M.
Development 120, 1325-1333, 1994
A;Title: Cortical granule biogenesis is active throughout oogenesis in sea urchins.
A;Reference number: Z20803; MUID:94298531; PMID:8026340
A;Accession: T30274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1297 <LAI>
A;Cross-references: UNIPROT:Q26632; UNIPARC:UPI0000081356; EMBL:U57753; NID:g1373379; PI

  Query Match             6.0%;  Score 143;  DB 2;  Length 1297;
  Best Local Similarity   23.1%;  Pred. No. 0.018;
  Matches  102;  Conservative   41;  Mismatches  179;  Indels  120;  Gaps   27;

Qy         47 TSCDSG---LGCQDTLML-----IESGPQVSLVLSK-----GCTEAKDQE---PRVT--- 87
              : | :|   :||  |::      :: |    :| ||       |:  :|:    | :
Db        610 SDCSNGQDEIGCPPTIVTCPAGRVDCGNNYCVVGSKCDGVSDCSNGQDESGCPPTIVTCP 669

Qy         88 EHRMGPGLSLISYTFVCRQEDFCNNLVNSLP-----LWAPQPPADPGSLRCPV---CLSM 139
               |:  |          |     |:|  : :      :  |    | |:  | |   |  :
Db        670 PGRIDCGTDYCVVGARCDGVSDCSNGQDEIGCPPTIVTCPAGRVDCGNNYCVVGSKCDGV 729

Qy        140 EGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQG--CMPQPGCNLLNGTQEIGPV 197
               |  |  |  || |: | :|  |:  |   :|  | |  |     |:  || | |
Db        730 SDCSNGQDESGCPPTTSACPEG--RVDCG---NNYCVVGSKCDGVSDCS--NGQDESGCP 782

Qy        198 GMTENC--NRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEM--------CEVGQVCQET 247
               |  |   | |  |  ||      :| :   |:        |  |:|
Db        783 PTTSTCPEGRVD---C--GTDYCVFGARCDGVSDCSNGQDEIGCPPTIVTCPAGRV---- 833

Qy        248 LLLIDVGLTSTLVGTK-----GCSTVGAQNSQKTTIHSAPPGVLVASYTHFC-------- 294
                | |    :||:|      ||  |   |:     || |   |    ::|
Db        834 ----DCGNNYCVVGSKCDGVSDCSN-GQDESECPPTTSACPEGRVDCGNNYCVVGGKCDG 888

Qy        295 SSDLCNSASSSSVLLNSLPPQAAPVPGDR-QCPT--CV-----QPLGTCSSGSPR----- 341
              ||  |    |       ||      | | | |  ||       :  ||:|
Db        889 VSDCSNGQDES-----GCPPTIVTCPAGRIDCGTNYCVVGARCDGVSDCSNGQDESGCPP 943

Qy        342 --MTCPRGATHCYDGYIHLSG-----GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSARE 394
               :||| |   | : |  :          |     :||                 | |
Db        944 AIVTCPAGRVDCGNNYCVVGSKCDGVSDCSNGQDEEGC--------------SFSSCRS 988

Qy        395 KRDVQPPASQHEGGGAEGLESL 416
               : |        |  | | :|||
Db        989 RGDC-------EFFGTEAVESL 1003


RESULT 3
JN0561
urokinase-type plasminogen activator receptor precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: JN0561; I46977
R;Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
Gene 125, 177-183, 1993
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and induc
A;Reference number: JN0560; MUID:93216119; PMID:8385052
A;Accession: JN0561
A;Molecule type: mRNA
A;Residues: 1-330 <KRA>
A;Cross-references: UNIPROT:Q05588; UNIPARC:UPI0000137CC6; GB:L03545; NID:g163802; PIDN
R;Reuning, U.; Little, S.P.; Dixon, E.P.; Johnstone, E.M.; Bang, N.U.
Thromb. Res. 72, 59-70, 1993
A;Title: Molecular cloning of cDNA for the bovine urokinase-type plasminogen activator
A;Reference number: I46977; MUID:94167671; PMID:8122188
A;Accession: I46977
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-330 <REU>
A;Cross-references: UNIPARC:UPI0000137CC6; GB:S70635; NID:g545770; PIDN:AAB30120.1; PID
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linka
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-300/Product: urokinase-type plasminogen activator receptor #status predicted <MAT>
F;21-104/Domain: Ly-6 homology <LY6A>
F;113-201/Domain: Ly-6 homology <LY6B>
F;209-296/Domain: Ly-6 homology <LY6C>
F;301-330/Domain: carboxyl-terminal propeptide #status predicted <CPRO>
F;28,72,179,189,279/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;300/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature for

  Query Match             6.0%;  Score 142;  DB 1;  Length 330;
  Best Local Similarity   21.3%;  Pred. No. 0.0051;
  Matches   95;  Conservative   43;  Mismatches  161;  Indels  146;  Gaps   22;

Qy          4 VLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLG-CQDTLMLI 62
              :||| :  :|    |:: | |:  |   |                  |  |   |: |:: :
Db          6 LLLLLVYTYIPGSWGLRCLQCENTTSCSV-------------EECTPGQDLCRTTVLSV 51

Qy         63 ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAP 122
               |      |: ||||   |:  |   :|     :  :| | |||  | ||          |
Db         52 WEGGNEMNVVRKGCTH-PDKTNRSMSYRAADQIITLSET-VCR-SDLCNK---------P 99

Qy        123 QPPADP-----GSLRCPVCLSME-GCLEGTTEEI-CPKGTTHCYDGL----LRLRGGGIF 171
               | |         | |  | | :  |  |  : : | |    | | :    |:   |
Db        100 NPGRDATVSRNRYLECASCSSTDLSCERGWDQTMQCLKSRDQCVDVITHRSLKENPG--- 156

Qy        172 SNLRVQGCMPQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWT 231
                ::||   |||          || |   | :   || |
Db        157 DERHIRGCGILPGCP--------GPTGFHNN-HTFHFLRC--------------------- 187

Qy        232 TSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVL----- 286
               ||  |  | | :                                : : ||  |
Db        188 -CNTTKCNAGSVLE-------------------------------LQNLPPNGLQCYSC 214

Qy        287 VASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPR 346
               :  | |||:        : |::   |           |::  ||    :|  |
Db        215 EGNGAHRCSSE-------ETFLIDCRGPM----------NQCLEATGTKGLRNPSYTIRG 257

Qy        347 GATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHE 406
               |   :  :|::     | :::  |          ||            || ||
Db        258 CAAPSWCQSLHVAEAFDLTHVNVSCCTGSG----CNH----------PARDDQPGK---- 299

Qy        407 GGGAEGLE--SLTWGVGLALAPALW 429
               |||       |:: | | |   ||
Db        300 -GGAPKTSPAHLSFFVSLLLTARLW 323


RESULT 4
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16840
R;Geisel, C.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid T10E10.
A;Reference number: Z18588
A;Accession: T16840
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Residues: 1-1101 <GEI>
A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339; PI
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T10E10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

  Query Match             5.7%;  Score 136.5;  DB 2;  Length 1101;
  Best Local Similarity   22.2%;  Pred. No. 0.044;
  Matches   88;  Conservative   44;  Mismatches  164;  Indels  101;  Gaps   23;

Qy         34 KVSDLPRQWTPK---NTSCDSGLGCQDTLML---IESGPQVSLVLSKGCTEAKDQEPRVT 87
Db        463 KITLCPGSYSPPFGVCGSCPSGTQCNQQLQMCCPLQQQPSTDIVYNV-VLLCPDGTPSTT 521

Qy         88 EHRMGPGLSLISYTFVC---------RQEDFCNNLVNSLPLWAPQPPADPGSLRCPVC-- 136
Db        522 SCSKGCGPNNACFQGACCPIRCPVGQNAVGFCSSGSCGVGSCYSKTTCCQEPIKLPVCSN 581

Qy        137 --LSMEGCLE----GTTEE----------ICPKGTT---------------HCYDGLLRL 165
Db        582 GMISQKRCLVAAECGLNLECSNGGCCPIPFCPNGVTARGRCSQVNGCPMGQACMEGL--- 638

Qy        166 RGGGIFSNLRVQGCMPQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGT--TIMTHGNL 223
Db        639 ------------CCPLPKCS--NGITSLGICTRTLDCGRIG-VDCNNGACCPLPTCPNN 682

Qy        224 AQEPTDWTTSNTEMCEVGQVCQETLLL---------IDVGLTSTLVGT------KGCSTV 268
Db        683 IASSQRCSGGCTNCCPVGQTCMNGGCCDLPSCPSGGFAISMCTGKCGTGFECVNSGCCSL 742

Qy        269 -----GAQNSQKTTIH-SAPPGVLVASYTHFCSSDLCNSAS-SSSV--LLNSLPPQAAPV 319
Db        743 PRCPSGLMSVQRCAMGIGCPPGNQCENGV-CCPMPMCSSGSIASSVCGMANSCP--IGYI 799

Qy        320 PGDRQCPTCVQPLGTC-SSGSPRMTCPRGATHCYDGY 355
Db        800 CEGRGC--CLEPLPLCPNGGRASMRCYRGA-ECPPGY 833


RESULT 5
A46019
notch-1 protein - mouse
N;Alternate names: motch protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid
Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
A;Reference number: A46019; MUID:93194170; PMID:8449489
A;Accession: A46019
A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2531 <DEL>
A;Cross-references: UNIPROT:Q01705; UNIPARC:UPI0000002922B; GB:Z11886; GB:S47228; NID:g28
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
submitted to the EMBL Data Library, April 1992
A;Description: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggest
A;Reference number: S25144
A;Accession: S25144
A;Molecule type: mRNA
A;Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRA>
A;Cross-references: UNIPARC:UPI0000177461; EMBL:Z11886
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety o
A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: C49175
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1161-1547 <LAR>
A;Cross-references: UNIPARC:UPI0000177462; EMBL:X68278; NID:g287987; PIDN:CAA48339.1;
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126159)
R;Kopan, R.; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A;Title: Mouse notch: expression in hair follicles correlates with cell fate determina
A;Reference number: A46438; MUID:93252998; PMID:8486742
A;Accession: B46438
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1865-1932,'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',20
A;Cross-references: UNIPARC:UPI0000177463
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C;Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision bet
C;Genetics:
A;Gene: notch-1
A;Map position: 2
A;Note: proximal region of chromosome 2
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;106-138/Domain: EGF homology <EGF1>
F;144-175/Domain: EGF homology <EG01>
F;222-254/Domain: EGF homology <EGF2>
F;261-292/Domain: EGF homology <EG02>
F;339-370/Domain: EGF homology <EG03>
F;416-449/Domain: EGF homology <EGF3>
F;456-487/Domain: EGF homology <EG04>
F;494-525/Domain: EGF homology <EG05>
F;532-563/Domain: EGF homology <EG06>
F;607-638/Domain: EGF homology <EG07>
F;682-713/Domain: EGF homology <EG08>
F;757-788/Domain: EGF homology <EG09>
F;795-826/Domain: EGF homology <EG10>
F;873-904/Domain: EGF homology <EG11>
F;911-942/Domain: EGF homology <EG12>
F;949-980/Domain: EGF homology <EG13>
F;987-1018/Domain: EGF homology <EG14>
F;1025-1056/Domain: EGF homology <EG15>
F;1063-1094/Domain: EGF homology <EG16>
F;1149-1180/Domain: EGF homology <EG17>
F;1187-1218/Domain: EGF homology <EG18>
F;1233-1264/Domain: EGF homology <EGF4>
F;1352-1383/Domain: EGF homology <EG19>
F;1391-1425/Domain: EGF homology <EGF>
F;1917-1948/Domain: ankyrin repeat homology <AN1>
F;1949-1981/Domain: ankyrin repeat homology <AN2>
F;1983-2015/Domain: ankyrin repeat homology <AN3>
F;2016-2048/Domain: ankyrin repeat homology <AN4>
F;2049-2081/Domain: ankyrin repeat homology <AN5>

  Query Match             5.7%;  Score 136.5;  DB 2;  Length 2531;
  Best Local Similarity   23.3%;  Pred. No. 0.11;
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Qy         86 VTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPADPGSLRCPVCLSMEG---- 141
Db        179 VNECSQNPGL--------CRHGGHCHNEI-------------GSYRCACCATHTGPHCE 216

Qy        142 ----------CLEGTTEEIC-PKG-TTH---CYDGLLRLRGGGIFSNLRVQGCMPQPGCN 186
Db        217 LPYVPCSPSPCQNGAT---CRPTGDTTHECACLPGF-----AGQNCEENVDDC---PGNN 265

Qy        187 LLNGTQEIGPVGMTENCN----------RKDFLTC--------HRGTTIMTHGNL-AQEP 227
Db        266 CKNGGACVDGVN-TYNCRCPPEVTGQYCTEDVDECQLMPNACQNAGTCHNTHGGYNCVCV 324

Qy        228 TDWTTSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIH-------- 279
Db        325 NGWT---------GEDCSENI-------------DDCAS--AACFQGATCHDRVASFYC 359

Qy        280 SAPPG--VLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQC--------PTCV 329
```

```
Db        360 ECPHGRTGLLCHLKHACISNPCNEGSNC---------DTNPVNGKRICTCPSGYTGPACS 410

Qy        330 QPLGTCSSGSPRM--------TCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLL 381
              | :  |  |: |         |        |  ||      |   :: :  |:: |
Db        411 QDVDECDLGANRCEHAGKCLNTLGSFECQCLQGYT-----GPGCEIDVNECISNPCQNDA 465

Qy        382 NHTRQIGIF 390
                |||  |
Db        466 TCLDQIGEF 474
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RESULT 6
VWHU
von Willebrand factor precursor - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A34480; S02377; A37139; S23676; A25298; A25469; A25366; S23618; S23645; A94
R;Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora
J. Biol. Chem. 264, 19514-19527, 1989
A;Title: Structure of the gene for human von Willebrand factor.
A;Reference number: A34480; MUID:90062044; PMID:2584182
A;Accession: A34480
A;Molecule type: DNA
A;Residues: 1-2813 <MAN>
A;Cross-references: UNIPROT:P04275; UNIPARC:UPI0000046823; EMBL:M25864
R;Bonthron, D.; Orkin, S.H.
Eur. J. Biochem. 171, 51-57, 1988
A;Title: The human von Willebrand factor gene. Structure of the 5' region.
A;Reference number: S02377; MUID:88111704; PMID:2828057
A;Accession: S02377
A;Molecule type: DNA
A;Residues: 1-177 <BO2>
A;Cross-references: UNIPARC:UPI000017431A; EMBL:X06828
R;Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sora
Biochemistry 30, 253-269, 1991
A;Title: Human von Willebrand factor gene and pseudogene: structural analysis and differ
A;Reference number: A37139; MUID:91105089; PMID:1988024
A;Accession: A37139
A;Molecule type: DNA
A;Residues: 990-1947 <MAD>
A;Cross-references: UNIPARC:UPI000016B30B; GB:M60675; NID:g340357; PIDN:AAA61295.1; PID:
A;Note: the authors translated the codon CGC for residue 156 as Gln
R;Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian,
Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
A;Title: Molecular cloning of the human gene for von Willebrand factor and identificatic
A;Reference number: S23676; MUID:87260814; PMID:3496594
A;Accession: S23676
A;Molecule type: DNA
A;Residues: 2731-2813 <COL>
A;Cross-references: UNIPARC:UPI000014240A; EMBL:M16945
R;Bonthron, D.; Orr, E.C.; Mitsock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
Nucleic Acids Res. 14, 7125-7127, 1986
A;Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
A;Reference number: A25298; MUID:87016349; PMID:3489923
A;Accession: A25298
A;Molecule type: mRNA
A;Residues: 1-470,'V',472-2813 <BON>
A;Cross-references: UNIPARC:UPI000017431B; EMBL:X04385
R;Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 1839-1847, 1986
A;Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protei
A;Reference number: A91044; MUID:87004550; PMID:3019665
A;Accession: A25469
A;Molecule type: mRNA
A;Residues: 1-470,'V',472-483,'R',485-1022,'K',1024-1025,'E',1027-1400 <VER>
A;Cross-references: UNIPARC:UPI000017431C; EMBL:X04146
A;Note: this sequence has been revised in reference A91056
R;Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 3074, 1986
A;Reference number: A91056
A;Accession: A25366
A;Molecule type: mRNA
A;Residues: 1021-1030 <VE2>
A;Cross-references: UNIPARC:UPI000017431D
A;Note: this is a revision to the sequence from reference A91044
R;Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
Biochem. Biophys. Res. Commun. 144, 657-665, 1987
A;Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeate
A;Reference number: S23618; MUID:87213253; PMID:3495266
A;Accession: S23618
A;Molecule type: mRNA
A;Residues: 1-120 <SH2>
A;Cross-references: UNIPARC:UPI000016B30A; EMBL:M17588; NID:g799330; PIDN:AAA65940.1; P
A;Accession: S23645
A;Molecule type: protein
A;Residues: 23-56 <SH3>
A;Cross-references: UNIPARC:UPI000017431E
R;Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
A;Title: Cloning and characterization of two cDNAs coding for human von Willebrand fact
A;Reference number: A94060; MUID:86016708; PMID:2864688
A;Accession: A94060
A;Molecule type: mRNA
A;Residues: 'WA',739,'C',744-769,'H',771-788,'A',790-803,'S',805-873;1289-1471,'D',1473
A;Cross-references: UNIPARC:UPI000017431F; UNIPARC:UPI0000174320
A;Note: the authors translated the codon TCG for residue 2168 as Cys
R;Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
Biochemistry 25, 3164-3171, 1986
A;Title: cDNA sequences for human von Willebrand factor reveal five types of repeated d
A;Reference number: A90504; MUID:86269894; PMID:3488076
A;Accession: A90504
A;Molecule type: mRNA
A;Residues: 781-788,'A',790-1424 <SHE>
A;Cross-references: UNIPARC:UPI0000174321
A;Note: 852-Gln, 857-Asp, and 1381-Thr were also found
R;Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.;
Science 228, 1401-1406, 1985
A;Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clone
A;Reference number: A44178; MUID:85244588; PMID:3874428
A;Accession: A44178
A;Molecule type: mRNA
A;Residues: 2621-2813 <GIN>
A;Cross-references: UNIPARC:UPI000016B307; EMBL:K03028; NID:g340308; PIDN:AAA61293.1; P
R;Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; v
Nucleic Acids Res. 13, 4699-4717, 1985
A;Title: Construction of cDNA coding for human von Willebrand factor using antibody pro
A;Reference number: S07363; MUID:85269603; PMID:3875078
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 2731-2813 <VE3>
A;Cross-references: UNIPARC:UPI000014240A; EMBL:X02672; NID:g37939; PIDN:CAA26503.1; PI
R;Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Livi
Cell 41, 49-56, 1985
A;Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a
A;Reference number: S23678; MUID:85201687; PMID:3873280
A;Accession: S23678
A;Molecule type: mRNA
A;Residues: 2731-2813 <LYN>
A;Cross-references: UNIPARC:UPI000014240A; EMBL:K03028
R;Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.
Biochemistry 25, 3171-3184, 1986
A;Title: Amino acid sequences of human von Willebrand factor.
A;Reference number: A90505; MUID:86269895; PMID:3524673
A;Accession: A90505
A;Molecule type: protein
A;Residues: 764-788,'A',790-1471,'D',1473-2813 <TIT>
A;Cross-references: UNIPARC:UPI0000174322
A;Note: 789-Thr was also found
R;Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
Biochemistry 25, 3146-3155, 1986
A;Title: Human von Willebrand factor: a multivalent protein composed of identical subun
A;Reference number: A23464; MUID:86269892; PMID:3015199
A;Accession: A23464
A;Molecule type: protein
A;Residues: 764-773;2803-2813 <CHO>
A;Cross-references: UNIPARC:UPI0000174323; UNIPARC:UPI0000174324

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R;Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
A;Title: Identification of a cleavage site directing the immunochemical detection of mol
A;Reference number: A36013; MUID:90349604; PMID:2385594
A;Accession: A36013
A;Molecule type: protein
A;Residues: 1606-1617 <DEN>
A;Cross-references: UNIPARC:UPI0000174325
R;Fay, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.;
Science 232, 995-998, 1986
A;Title: Propolypeptide of von Willebrand factor circulates in blood and is identical to
A;Reference number: A60913; MUID:86208144; PMID:3486471
A;Accession: A60913
A;Molecule type: protein
A;Residues: 576-590 <FAY>
A;Cross-references: UNIPARC:UPI0000174326
C;Genetics:
A;Gene: GDB:VWF
A;Cross-references: GDB:119125; OMIM:193400
A;Map position: 12p13.3-12p13.2
A;Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 478/1; 51
5/1; 1724/1; 1771/1; 1819/1; 1874/1; 1888/3; 1948/1; 2021/3; 2086/1; 2200/1; 2266/3; 230
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
C;Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-763/Product: von Willebrand antigen II #status predicted <MA1>
F;34-386/Domain: type D repeat 1 <DD1>
F;387-745/Domain: type D repeat 2 <DD2>
F;698-700/Region: cell attachment (R-G-D) motif
F;764-2813/Product: von Willebrand factor #status predicted <MA2>
F;784-865/Domain: D' <DDD>
F;788-833,2216-2261/Region: duplication
F;826-853,2400-2515,2544-2662/Region: duplication
F;842-1130,1934-2203/Region: duplication
F;866-1241/Domain: type D repeat 3 <DD3>
F;1275-1443/Domain: von Willebrand factor type A repeat homology <VWA1>
F;1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>
F;1947-2295/Domain: type D repeat 4 <DD4>
F;2296-2330/Domain: type B repeat 1 <VB1>
F;2340-2365/Domain: type B repeat 2 <VB2>
F;2375-2399/Domain: type B repeat 3 <VB3>
F;2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>
F;2507-2509/Region: cell attachment (R-G-D) motif
F;2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
F;857,1231,1515,1574,2223,2290,2357,2400,2546,2585,2790/Binding site: carbohydrate (Asn)
F;1147/Binding site: carbohydrate (Asn) (covalent) #status atypical
F;1248,1255,1256,1468,1477,1487,1679,2298/Binding site: carbohydrate (Thr) (covalent) #s
F;1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

  Query Match             5.5%;  Score 131.5;  DB 1;  Length 2813;
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  Matches   85;  Conservative   39;  Mismatches  132;  Indels  135;  Gaps   23;

Qy         18 GVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTL----------MLIE 63
Db       2092 GANDFMLRDGTVTTDWKT--LVQEWTVQR----PGQTCQPILEEQCLVPDSSHCQVLLLP 2145

Qy         64 SGPQVSLVLSKG-----CTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLP 118
Db       2146 LFAECHKVLAPATFYAICQQDSCHQEQVCE-------VIASYAHLCRTNGVCVD------ 2192

Qy        119 LWAPQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGG----GIF--- 171
Db       2193 -WR---TPDFCAMSCPPSLVYNHCEHG-----CPR---HC-DGNVSSCGDHPSEGCFCPP 2239

Qy        172 SNLRVQG-CMPQPGCNLLNGTQEIGPVGMTENCNRKDFL----------TCHRGTTI 217
Db       2240 DKVMLEGSCVPEEAC-----TQCIGEDGV-----QHQFLEAWVPDHQPCQICTCLSGRKV 2289

Qy        218 MTHGNLAQEPTDWTTSNT-EMCEVG-------QVCQETLLLIDV----------GLT 256
Db       2290 ----NCTTQPCPTAKAPTCGLCEVARLRQNADQCCPEYECVCDPVSCDLPPVPHCERGLQ 2345

Qy        257 STLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQA 316
Db       2346 PTLTN----------PGECRPNFTCACRKEECKRVSPP-----SCPPHR 2379

Qy        317 APVPGDRQCPTCVQPLGTCSSGSPRMTCPRG 347
Db       2380 LPTLRKTQC--CDEYECACNCVNSTVSCPLG 2408


RESULT 7
T15840
hypothetical protein C54G7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15840
R;Du, Z.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C54G7.
A;Reference number: Z18416
A;Accession: T15840
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2946 <DUZ>
A;Cross-references: UNIPARC:UPI000017B871; EMBL:U40410; NID:g1065453; PID:g1065455; PID
C;Genetics:
A;Gene: CESP:C54G7.3
A;Introns: 16/1; 53/2; 92/1; 160/3; 295/1; 346/1; 392/1; 440/1; 475/3; 579/1; 615/3; 1
46/1; 2561/2; 2603/2; 2626/2; 2665/2; 2716/3; 2804/3; 2884/3

  Query Match             5.5%;  Score 130;  DB 2;  Length 2946;
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  Matches   98;  Conservative   52;  Mismatches  202;  Indels   98;  Gaps   24;

Qy         23 LCQFGTVQHVWKVSDLPRQWTPKNTSCDS------GLGCQDTLMLIESGPQVSLVLSKGC 76
Db       1683 MCKFGDV----KCDPSEPVTSPPGGSCSNLRECTGGSVCREGWCIC---PDPSMIVNRGI 1735

Qy         77 TEAKDQEPRVTEHRMGPGLSL---------ISYTFVCRQEDFCNNLVNSLPLWAPQ-PPA 126
Db       1736 CIQSGPKPTLPPRTPIPQVPLPPQLPISVHVPQVTITKAQPF----ITEAPL-APQGKKI 1790

Qy        127 DPGSLRC---PVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQP 183
Db       1791 VPGG-RCGPIDVCVGGSNCIEGFC--LCPAGQQPSNSGRCEK-----FTTTSRQTTLPST 1842

Qy        184 GCNLLNGTQEIGPVGMTE--NCNRKDFLTCHRGTT---IMTHGNL---AQEPTDWTTSNT 235
Db       1843 TTTQGTTTTTTAPPPTTSVFSFTIADLLSTRRQPAFIEIPTHVPLTTTAIQTDDECTAIG 1902

Qy        236 EMCEVGQVCQ-------ETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTT-IHSAP----- 282
Db       1903 LICKGNTVCRNKSCQCPETYVLHHDGCVSPEEAARRKARGKARHEATTARLYSKPGESCT 1962

Qy        283 -----PGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSS 337
Db       1963 QGQTCVGGSACSFRKLCECPQDKSEISQGQCVT--PRKLEVVPG----ASC-NANTVCTK 2015

Qy        338 GSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRD 397
Db       2016 GS---TCESGLCRCQPGYIAVSG----------NCVALPMS----------TTPKMRV 2050

Qy        398 VQPPASQHEGG-GAEGLESLTWGVGLALAP 426
Db       2051 IAKPLESCENGETCEGGSNCDYDTGICMCP 2080


RESULT 8
S16148
gene serrate protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16148; S16878; A36666
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R;Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a cc
A;Reference number: S16148; MUID:91347903; PMID:1840519
A;Accession: S16148
A;Molecule type: mRNA
A;Residues: 1-1408 <THO1>
A;Cross-references: UNIPROT:P18168; UNIPARC:UPI000017A1AA; EMBL:X56811
R;Thomas, U.
submitted to the EMBL Data Library, November 1990
A;Reference number: S16878
A;Accession: S16878
A;Molecule type: mRNA
A;Residues: 1-1351,'T',1353-1408 <THO2>
A;Cross-references: UNIPARC:UPI000013588E; EMBL:X56811; NID:g8563; PID:g8564
R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential fc
A;Reference number: A36666; MUID:91099666; PMID:2125287
A;Accession: A36666
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15,20-26,'A',28-1408 <FLE>
A;Cross-references: UNIPARC:UPI00000498BA; GB:M35759; NID:g158605; PID:g158606
C;Genetics:
A;Gene: FlyBase:Ser
A;Cross-references: FlyBase:FBgn0004197
C;Keywords: glycoprotein; transmembrane protein
F;1-84/Domain: signal sequence #status predicted <SIG>
F;85-1408/Product: gene serrate protein #status predicted <MAT>
F;85-1221/Domain: extracellular #status predicted <EXT>
F;283-316/Domain: EGF homology <EG01>
F;319-348/Domain: EGF homology <EG02>
F;355-388/Domain: EGF homology <EG03>
F;395-488/Domain: EGF homology #status atypical <EG04>
F;495-526/Domain: EGF homology <EG05>
F;533-608/Domain: EGF homology #status atypical <EG06>
F;615-645/Domain: EGF homology <EG07>
F;652-683/Domain: EGF homology <EG08>
F;690-720/Domain: EGF homology <EG09>
F;727-796/Domain: EGF homology #status atypical <EG10>
F;803-834/Domain: EGF homology <EG11>
F;841-876/Domain: EGF homology <EG12>
F;883-914/Domain: EGF homology <EG13>
F;921-952/Domain: EGF homology <EG14>
F;997-1060/Region: cysteine-rich
F;1222-1246/Domain: transmembrane #status predicted <TM1>
F;1247-1408/Domain: intracellular #status predicted <INT>
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn

  Query Match             5.4%;  Score 128;  DB 2;  Length 1408;
  Best Local Similarity   21.7%;  Pred. No. 0.24;
  Matches  108;  Conservative   34;  Mismatches  168;  Indels  188;  Gaps   29;

Qy          43 TPKNTSCD-----SGLGCQDTLMLIESGP-------QVSLVLSKGCTEAKDQEPRVTEHR 90
               ||:   |       :|  |:    |    |         |||  |   |          |
Db         703 TPEGYYCHCPPDRAGKHCEQLRPLCSQPPCNEGCFANVSLATSATTTTTTTTTATTTRKM 762

Qy          91 MGPGLSLISYTFVCRQED--------------FCNNLVNSLPLWAPQPPADPGSLRCPVC 136
               |     |    |  |                || : :|     :| |  : |      :|
Db         763 AKPSGLPCSGHGSCEMSDVGTFCKCHVGHTGTFCEHNLNEC---SPNPCRNGG-----IC 814

Qy         137 LSMEG-----CLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMP-------QPG 184
               |  :|     |: | | : | :  | || |  : : ||         |||        ||
Db         815 LDGDGDFTCECMSGWTGKRCSERATGCYAG--QCQNGGT--------CMPGAPDKALQPH 864

Qy         185 CNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDW------------T 231
               |     |   :       : | :    || | |         :    |
Db         865 CRCAPGWTGLFCAEAIDQCRGQ---PCHNGGT-------CESGAGWFRCVCAQGFSGPDC 914

Qy         232 TSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPG------- 284
                 |   |   | ||      ||         |  | | :             |||
Db         915 RINVNECS-PQPCQGGATCID--------GIGGYSCI------------CPPGRHGLRCE 953

Qy         285 VLVASYTHFCSSDLCNSASSSSVLLNSLPPQAA--------------PVPGDRQCPTCVQ 330
               :|::           | :||       |:: |  |                  |  |  ||
Db         954 ILLSD-----PKSACQNAS------NTISPYTALNRSQNWLDIALTGRTEDDENCNACV- 1001

Qy         331 PLGTCSSGSPRMT---CPRGATHCYDGYIHLSGGGLSTKMSIQG-------CVAQPSSFL 380
                   | :|: | |    |  |  :||          ||    :: |          ||   |
Db        1002 ----CENGTSRCTNLWC--GLPNCY------KVDPLSKSSNLSGVCKQHEVCVPALSETC 1049

Qy         381 LNHTRQI-GIFSARE-KRDVQPP-------------------------ASQHEGGGA-- 410
               |:    : |   | |  | | ||                        | :  | ||
Db        1050 LSSPCNVRGDCRALEPSRRVAPPRLPAKSSCWPNQAVVNENCARLTILLALERVGKGASV 1109

Qy         411 EGLESLTWGVGLALAPAL 428
               ||| ||   | : ||  |
Db        1110 EGLCSL---VRVLLAAQL 1124


RESULT 9
T15881
hypothetical protein D1044.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15881
R;Pauley, A.
submitted to the EMBL Data Library, June 1994
A;Description: The sequence of C. elegans cosmid D1044.
A;Reference number: Z18423
A;Accession: T15881
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1895 <PAU>
A;Cross-references: UNIPARC:UPI000004CAE8; EMBL:U00065; NID:g495681; PID:g495684; PIDN:
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:D1044.3
A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2; 1

  Query Match             5.4%;  Score 127.5;  DB 2;  Length 1895;
  Best Local Similarity   20.6%;  Pred. No. 0.35;
  Matches   73;  Conservative   51;  Mismatches  148;  Indels   83;  Gaps   15;

Qy          22 LLCQFGTVQHVWKVSDLPRQWTPKNTSC----DSGLGCQDTLMLIESGPQVSLVLSKGCT 77
               | || ||| :               |: |      |  ||  :   |::    |: ::: ||
Db        1121 LNCQLGTVSY-------------NSQCITLASPGQNCQTSSQCIDN----SVCMNQMCT 1162

Qy          78 EAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPADPGSLRCPVCL 137
                  :       :|:  |  :   : :|:|      |||:  :           |:    |:
Db        1163 CNNN-------YRLVYGYCVPITSSICQQ---TQTLVNNQCVLL--------SIVGETCI 1204

Qy         138 SMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCN---------LL 188
               : : |: |    :|  ||  | :|    : |  | |:           ||
Db        1205 ANQQCVGGA---MCNSGTCQCTNGATAMYGYCISSS--------SSSCNSNQVSINGMCY 1253

Qy         189 NGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL 248
               |  |  |    :: |       |     : |  :::             |   |||
Db        1254 NTVQVGGSCSFSQQCLNN--AVCTNNICVSTFCSVS------------CSTNQVCISNQ 1298

Qy         249 LLIDVGLTSTLVGTKGCSTVGAQNSQ-KTTIHSAPPGVLVASYTHFCSSDLCNSASSSSV 307
               | : |  ||:: |       |||  ::|   | |   ::     :::  |    : |
Db        1299 CYNYVSIGSQCVGSQQC----LSNSQCISSICQCPQGTQQSNGVCTGNNNNNNQCQPNQV 1354

Qy         308 LLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGG 362
               |:|:    :    ||   | ||     :    || |:|:  :||      |
Db        1355 LINNQCYNTVSI--GFQCQFPQQCLGNSQCMNSMCQCPTGSTN-VNGYCQGGSNG 1406


RESULT 10
T30075
hypothetical protein F57F4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30075
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```
R;Miller, N.; Bradshaw, H.
submitted to the EMBL Data Library, September 1996
A;Description: The sequence of C. elegans cosmid F57F4.
A;Reference number: Z20730
A;Accession: T30075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2090 <MIL>
A;Cross-references: UNIPROT:Q94247; UNIPARC:UPI000007C44F; EMBL:U70856; PIDN:AAB09167.1;
A;Experimental source: strain Bristol N2; clone F57F4
C;Genetics:
A;Gene: CESP:F57F4.4
A;Map position: 5
A;Introns: 42/3; 117/2; 1962/3; 2025/1

  Query Match             5.3%;  Score 126.5;  DB 2;  Length 2090;
  Best Local Similarity   17.1%;  Pred. No. 0.46;
  Matches   77;  Conservative   60;  Mismatches  182;  Indels  131;  Gaps   20;

Qy         44 PKNTSCDSGLGCQDTLMLIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFV 103
Db       1390 PPPTSVDYAIACY-TGLYVNGVPSTPVILG----ACQGQCASISLNTTLNGVATTATLYG 1444

Qy        104 CRQEDFCNNLVNSLPLWAPQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLL 163
Db       1445 CDPSTVCQSL--NMNNWCASP--IPGVSGC--CCNTDLCLDPPKNKTVPSGFRKCFAGIY 1498

Qy        164 ---RLRGGGIF--------------SNLRVQGCMPQPGCNLLNGTQEIGPVGMT------ 200
Db       1499 AQGKATGSEIFCPGKCASIQATLNQDPVAIFGCVPTQFCRQLEMYDECKPLPYDTTVTGC 1558

Qy        201 -----ENC------------------NRKDF-LTCHRGTTIMTHGNLAQEPTDW------ 230
Db       1559 CCDNYNNCNVDLAGYGGKINTSMPVTNFRDYPIACFSGLYV---NNMPISIAGWQACKGE 1615

Qy        231 --------------TTSNTEMCEVGQVCQE-----TLLLIDVGLTSTLVGTKGC------ 265
Db       1616 CASATLSTMYNGALTNATIYTCDPVSTCYQLGMNNNCTTIENGLSGCCCSTDACLDPTVS 1675

Qy        266 --------------------STVGAQ---NSQKTTIHSAPPGVLVASYTHFCSSDLCNSA 302
Db       1676 PPRTPNPLKCYVGLQSTYNSLSLGAETYCSGQCASLTGIVGGFNVTTY-HCVADTICKSL 1734

Qy        303 SSSSVLLNSLPPQAAPVPGDRQCPT-CVQPLGTCSSGSPRM-----TCPRGATHCYDGYI 356
Db       1735 --------EIKDTCRPLWSDREVTACCCNNADNCNLKDPNVKPGPAVLPDFPTACYQGLL 1786

Qy        357 HLSGGGLSTKMSIQGCVAQPSSFLLNHTRQ 386
Db       1787 -VNNQTYGAPLTLQGCYGDCASITISTTIQ 1815


RESULT 11
T30074
hypothetical protein F57F4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30074
R;Miller, N.; Bradshaw, H.
submitted to the EMBL Data Library, September 1996
A;Description: The sequence of C. elegans cosmid F57F4.
A;Reference number: Z20730
A;Accession: T30074
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2153 <MIL>
A;Cross-references: UNIPROT:Q94246; UNIPARC:UPI000007CB3D; EMBL:U70856; PIDN:AAB09166.1;
A;Experimental source: strain Bristol N2; clone F57F4
C;Genetics:
A;Gene: CESP:F57F4.3
A;Map position: 5
A;Introns: 42/3; 117/2; 1962/3; 2025/1

  Query Match             5.3%;  Score 126.5;  DB 2;  Length 2153;
  Best Local Similarity   17.1%;  Pred. No. 0.47;
  Matches   77;  Conservative   60;  Mismatches  182;  Indels  131;  Gaps   20;

Qy         44 PKNTSCDSGLGCQDTLMLIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFV 103
Db       1390 PPPTSVDYAIACY-TGLYVNGVPSTPVILG----ACQGQCASISLNTTLNGVATTATLYG 1444

Qy        104 CRQEDFCNNLVNSLPLWAPQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLL 163
Db       1445 CDPSTVCQSL--NMNNWCASP--IPGVSGC--CCNTDLCLDPPKNKTVPSGFRKCFAGIY 1498

Qy        164 ---RLRGGGIF--------------SNLRVQGCMPQPGCNLLNGTQEIGPVGMT------ 200
Db       1499 AQGKATGSEIFCPGKCASIQATLNQDPVAIFGCVPTQFCRQLEMYDECKPLPYDTTVTGC 1558

Qy        201 -----ENC------------------NRKDF-LTCHRGTTIMTHGNLAQEPTDW------ 230
Db       1559 CCDNYNNCNVDLAGYGGKINTSMPVTNFRDYPIACFSGLYV---NNMPISIAGWQACKGE 1615

Qy        231 --------------TTSNTEMCEVGQVCQE-----TLLLIDVGLTSTLVGTKGC------ 265
Db       1616 CASATLSTMYNGALTNATIYTCDPVSTCYQLGMNNNCTTIENGLSGCCCSTDACLDPTVS 1675

Qy        266 --------------------STVGAQ---NSQKTTIHSAPPGVLVASYTHFCSSDLCNSA 302
Db       1676 PPRTPNPLKCYVGLQSTYNSLSLGAETYCSGQCASLTGIVGGFNVTTY-HCVADTICKSL 1734

Qy        303 SSSSVLLNSLPPQAAPVPGDRQCPT-CVQPLGTCSSGSPRM-----TCPRGATHCYDGYI 356
Db       1735 --------EIKDTCRPLWSDREVTACCCNNADNCNLKDPNVKPGPAVLPDFPTACYQGLL 1786

Qy        357 HLSGGGLSTKMSIQGCVAQPSSFLLNHTRQ 386
Db       1787 -VNNQTYGAPLTLQGCYGDCASITISTTIQ 1815


RESULT 12
C42125
trophozoite cysteine-rich surface antigen 72 - Giardia lamblia (fragment)
N;Alternate names: CRP72
C;Species: Giardia lamblia
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: C42125
R;Adam, R.D.; Yang, Y.M.; Nash, T.E.
Mol. Cell. Biol. 12, 1194-1201, 1992
A;Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 g
A;Reference number: A42125; MUID:92186850; PMID:1545800
A;Accession: C42125
A;Molecule type: DNA
A;Residues: 1-677 <ADA>
A;Cross-references: UNIPROT:Q7M3R4; UNIPARC:UPI000017B5CF; GB:M83934; NID:g159123
A;Experimental source: trophozoites
A;Note: sequence extracted from NCBI backbone (NCBIN:88443, NCBIP:88444); this ORF is n
C;Keywords: surface antigen

  Query Match             5.1%;  Score 122.5;  DB 2;  Length 677;
  Best Local Similarity   20.9%;  Pred. No. 0.27;
  Matches   71;  Conservative   30;  Mismatches  121;  Indels  117;  Gaps   19;

Qy        107 EDFCNNLVNSLPLWAPQPPA-----------DPGSLRCPVC-----LSMEGC---LEGTT 147
Db         40 DGFCR------PFGSPQAAAAGCTKAGGAALDKMTATCEKCGDGYFLFMGGCYKTTDGPG 93

Qy        148 EEICPKG----TTHCYDGLLRLRGGGIFSNLRVQGCMPQPG-----CNLLNGTQEIGPVG 198
Db         94 SEICTKAEGGLCTEC------KTANGLFKN---PAATPEKGSECILCSDINGADGYTGVA 144

Qy        199 MTENCNR-----------------KDFLTCHR--GTTIMTHGNLAQEPT---------D 229
Db        145 NCAQCTKSDSNKGAATCTACQAGYYKDFQACSKCDGTCLTCETSAAQCTSCPEGKYLKGD 204

Qy        230 WTTSNTEMC----------------EVGQVCQETLLLIDVGLTSTLVGTKGCSTVGAQN 272
```

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Db        205 KSCVNNNGCTGNTYADPESGKCLPCNTIDQACTQ------CEVDSTTKKPK-CTNCGGQK 257

Qy        273 SQKTTIHSAPPGVLVASYTHFCS------SDLCNSASSSSVLLNSLPPQAAPVPGDRQCP 326

Db        258 MVKTAI----DGTTTCVDANGCATSNVDGSHFLNDGSTKCILCSD---DSESLEANKGTP 310

Qy        327 TCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLST 365

Db        311 GC----KTCKKNGAKPTC----SECLDGYYNSGNGGTVT 341


RESULT 13
T09059
notch4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:g2564945;
C;Genetics:
A;Gene: notch4
A;Map position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
1679/3; 1729/1; 1761/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology <EGF>

  Query Match             5.1%;  Score 122.5;  DB 2;  Length 1964;
  Best Local Similarity   20.4%;  Pred. No. 0.83;
  Matches  113;  Conservative   36;  Mismatches  161;  Indels  243;  Gaps   31;

Qy         17 PGVQALLCQFG---TVQH----------------------VWK-------VSDLPRQWTPK 45

Db        263 PGFTGLDCEMNPDDCVRHQCQNGATCLDGLDTYTCLCPKTWKGWDCSEDIDECEARGPPR 322

Qy         46 NTSCDSGLGCQDTLMLIESGPQVSLVLS----KGCTEAKDQEPRVTEHRMGPGLSLI--- 98

Db        323 ---CRNGGTCQNT-----AGSFHCVCVSGWGGAGCEENLDDCAAAT---CAPGSTCIDRV 371

Qy         99 -SYT---------FVCRQEDFC-------NNLVNSLPL---------------------- 119

Db        372 GSFSCLCPPGRTGLLCHLEDMCLSQPCHVNAQCSTNPLTGSTLCICQPGYSGSTCHQDLD 431

Qy        120 ---WAPQPPA----------DPGSLRCPVCLSMEGCLEGTT------------EEICPKG 154

Db        432 ECQMAQQGPSPCEHGGSCINTPGSFNCL-------CLPGYTGSRCEADHNECLSQPCHPG 484

Qy        155 TT--------HCY--DGLLRLRGGGIFSNLRVQGCMPQPGCN------LLNGTQEIGPVG 198

Db        485 STCLDLLATFHCLCPPGL-----EGRLCEVEVNECTSNPCLNQAACHDLLNGFQCLCLPG 539

Qy        199 MTENCNRKDFLTCHRGTTIMTHGNLAQEP-----------------TDWTTSNTEMCEVG 241

Db        540 FTGARCEKDMDEC-SSTPCANGGRCRDQPGAFYCECLPGFEGPHCEKEVDECLSDPCPVG 598

Qy        242 QVCQET----LLLIDVGLTSTLVGTKGCSTVGAQNSQKT--TIHSAPPGVLVASYTHFCS 295

Db        599 ASCLDLPGAFFCLCRPGFTGQLCEVPLCTPNMCQPGQQCQGQEHRAP-----------C- 646

Qy        296 SDLCNSASSSSVLLNSLPPQAAP--VPGDRQCP------------------------- 326

Db        647 --LC--------------PDGSPGCVPAEDNCPCHHGHCQRSLCVCDEGWTGPECETELG 690

Qy        327 -----------TC-VQPLG---TCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQG 371

Db        691 GCISTPCAHGGTCHPQPSGYNCTCPAGYMGLTCSEEVTACHSGPC-LNGGSCSIRPEGYS 749

Qy        372 CVAQPSSFLLNHT 384

Db        750 CTCLPS-----HT 757


RESULT 14
S40992
hypothetical protein K04H4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-May-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S40992
R;Ainscough, R.
submitted to the EMBL Data Library, October 1993
A;Reference number: S40991
A;Accession: S40992
A;Molecule type: DNA
A;Residues: 1-738 <AIN>
A;Cross-references: UNIPROT:P34504; UNIPARC:UPI000017BA8E; EMBL:Z27078
C;Genetics:
A;Introns: 62/1; 140/1; 206/1; 226/1; 269/1; 308/1; 536/1; 604/1; 668/1

  Query Match             5.1%;  Score 121.5;  DB 2;  Length 738;
  Best Local Similarity   20.3%;  Pred. No. 0.35;
  Matches   94;  Conservative   43;  Mismatches  170;  Indels  155;  Gaps   21;

Qy         48 SCDSGLGCQDTLMLIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQE 107

Db        329 TCSNGLCCAGTSTTVK-----------CLDGSDAVGACIPSCTGDGCGGVQVSYYCGSG 376

Qy        108 DFCNNLVNSLPLWAPQPPADPGSLRCPV--CLSMEGCLEGTTEEICPKGTT--------- 156

Db        377 YTCTT---------------GNICCPINSCPNGGEVLGPTINGLCPTGYTVQGNLCCSA 420

Qy        157 HCYDGLLRLRGGGIFSNLRVQG-CMPQPGCNLLNG---------TQEIG---------- 195

Db        421 TCTDGSTGLPS--------VNGVCI--DGYSLTNGVCCPASVTCTDEISIGPCTGTGFNG 470

Qy        196 --PVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQ----VCQETLL 249

Db        471 GCPAGYACDSNQVNCCPVVRYT------------------DESCQVGPAIDGLCPPGYV 511

Qy        250 LIDV------------GLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSD 297

Db        512 VVYIPNSPLITNGVNPGTCIDLQCTTGLCLTANQIGDCDTATDA--GTCPTGYTCFTNAG 569

Qy        298 LCNSASSSSVLLNSLPPQAAPVPG---------DRQCP---TCVQ---PLGTCSSG---- 338

Db        570 ICCSTTTFSRLRIGNSRQMAQKPNYGRPLHSYMPRKCPSGDTAVSGCFPNGSCGTGYECV 629

Qy        339 -SPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRD 397

Db        630 SSLNLCCPPGQPQTFPSFPGNNNG----------------FNINNNNRFGSLSMSPR-- 670

Qy        398 VQPPAS--QHEG---GGAEGLESLTWGVGLALAPALWWGVVC 434

Db        671 --PIGARCQLDGECVGQAEGLSMCHAGVCQCSPIAYTQGIAC 710


RESULT 15
B88553
protein K04H4.2b [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: B88553
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolc
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
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A;Accession: B88553
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-739 <STO>
A;Cross-references: UNIPARC:UPI000016415C; GB:chr_III; PIDN:CAA81588.1; PID:g3878238; GS
C;Genetics:
A;Gene: K04H4.2b
A;Map position: 3

  Query Match             5.1%;  Score 121.5;  DB 2;  Length 739;
  Best Local Similarity   20.3%;  Pred. No. 0.35;
  Matches   94;  Conservative   43;  Mismatches  170;  Indels  155;  Gaps   21;

Qy         48 SCDSGLGCQDTLMLIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQE 107
              :| :|| |  |    ::             | :  |          | |   :  :: |
Db        330 TCSNGLCCAGTSTTVK------------CLDGSDAVGACIPSCTGDGCGGVQVSYYCGSG 377

Qy        108 DFCNNLVNSLPLWAPQPPADPGSLRCPV--CLSMEGCLEGTTEEICPKGTT--------- 156
                |                |:: ||:  | :    |  |   :|| | |
Db        378 YTCTT----------------GNICCPINSCPNGGEVLGPTINGLCPTGYTVQGNLCCSA 421

Qy        157 HCYDGLLRLRGGGIFSNLRVQG-CMPQPGCNLLNG---------TQEIG----------- 195
              | ||   |          | | |:   | :| ||          | ||
Db        422 TCTDGSTGLPS--------VNGVCI--DGYSLTNGVCCPASVTCTDEISIGPCTGTGFNG 471

Qy        196 --PVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQ----VCQETLL 249
                | |   : |: :    | |                | |:||     :|    :
Db        472 GCPAGYACDSNQVNCCPVVRYT-----------------DESCQVGPAIDGLCPPGYV 512

Qy        250 LIDV-----------GLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSD 297
              :: :           |   | | |     |     |  | |     || | ::
Db        513 VVYIPNSPLITNGVNPGTCIDLQCTTGLCLTANQIGDCDTATDA--GTCPTGYTCFTNAG 570

Qy        298 LCNSASSSSVLLNSLPPQAAPVPG---------DRQCP---TCVQ---PLGTCSSG---- 338
              :| | :: | |       | |  |           |:||   | |    | |:| :|
Db        571 ICCSTTTFSRLRIGNSRQMAQKPNYGRPLHSYMPRKCPSGDTAVSGCFPNGSCGTGYECV 630

Qy        339 -SPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRD 397
               |  : || |    :  :   : |                | :|:  : |  |   :
Db        631 SSLNLCCPPGQPQTFPSFPGNNNG----------------FNINNNNRFGSLSMSPR-- 671

Qy        398 VQPPAS--QHEG---GGAEGLESLTWGVGLALAPALWWGVVC 434
                |  :  | :|   | ||||     ||       |   |: |
Db        672 --PIGARCQLDGECVGQAEGLSMCHAGVCQCSPIAYTQGIAC 711


Search completed: July 11, 2006, 09:30:40
Job time : 43 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:21:42 ; Search time 300 Seconds
(without alignments)
1347.439 Million cell updates/sec

Title: US-10-727-619-2
Perfect score: 2381
Sequence: 1 MSAVLLLALLGFILPLPGVQ.....WGVGLALAPALWWGVVCPSC 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2381	100.0	437	2	Q9HDA5_HUMAN	Q9hda5 homo sapien
2	2370	99.5	437	2	Q8N6Q3_HUMAN	Q8n6q3 homo sapien
3	2360	99.1	437	2	Q96QH1_HUMAN	Q96qh1 homo sapien
4	1179	49.5	817	2	Q8R2S8_MOUSE	Q8r2s8 mus musculu
5	1108	46.5	248	2	Q711Q2_HUMAN	Q711q2 homo sapien
6	687	28.9	145	2	Q8NCV9_HUMAN	Q8ncv9 homo sapien
7	523	22.0	212	2	Q9D0T8_MOUSE	Q9d0t8 mus musculu
8	378.5	15.9	246	2	Q810N3_MOUSE	Q810n3 mus musculu
9	366	15.4	153	2	Q78KC5_MOUSE	Q78kc5 mus musculu
10	341.5	14.3	249	2	Q9BPY7_HUMAN	Q9bpy7 homo sapien
11	341.5	14.3	267	2	Q7L5R2_HUMAN	Q7l5r2 homo sapien
12	330.5	13.9	267	2	Q9BY14_HUMAN	Q9by14 homo sapien
13	298.5	12.5	250	2	Q924B5_RAT	Q924b5 rattus norv
14	294	12.3	196	2	Q8CFJ5_MOUSE	Q8cfj5 mus musculu
15	293	12.3	253	2	Q7TQN2_CRIGR	Q7tqn2 cricetulus
16	282	11.8	250	2	Q9JMI7_MOUSE	Q9jmi7 mus musculu
17	252	10.6	246	1	LYPD4_MOUSE	Q8bvp6 mus musculu
18	247	10.4	246	1	LYPD4_BOVIN	Q32ld3 bos taurus
19	240	10.1	246	1	LYPD4_HUMAN	Q6uwn0 homo sapien
20	163	6.8	5376	1	ZAN_MOUSE	O88799 mus musculu
21	154	6.5	5374	2	Q99ND0_MOUSE	Q99nd0 mus musculu
22	152	6.4	1577	2	Q4SPE0_TETNG	Q4spe0 tetraodon n
23	148.5	6.2	1264	2	Q26632_STRPU	Q26632 strongyloce
24	145.5	6.1	1408	2	Q4RX38_TETNG	Q4rx38 tetraodon n
25	144.5	6.1	1637	2	Q9XSV8_BOVIN	Q9xsv8 bos taurus
26	144.5	6.1	5146	2	Q8SPM4_BOVIN	Q8spm4 bos taurus
27	143.5	6.0	4260	2	Q4T3T2_TETNG	Q4t3t2 tetraodon n
28	142	6.0	330	1	UPAR_BOVIN	Q05588 bos taurus
29	142	6.0	555	2	Q54RC6_DICDI	Q54rc6 dictyosteli
30	142	6.0	950	2	Q802C1_XENLA	Q802c1 xenopus lae
31	142	6.0	2602	2	Q7PSV8_ANOGA	Q7psv8 anopheles g
32	141.5	5.9	1280	2	Q6QHS1_LYTVA	Q6qhs1 lytechinus
33	141	5.9	555	1	DP87_DICDI	Q04503 dictyosteli
34	140.5	5.9	2428	2	Q8I6X6_BOOMI	Q8i6x6 boophilus m
35	139	5.8	1642	2	Q515F7_ENTHI	Q515f7 entamoeba h
36	139	5.8	2284	2	Q9VPG1_DROME	Q9vpg1 drosophila
37	138.5	5.8	1302	1	LTBP3_HUMAN	Q9ns15 homo sapien
38	138	5.8	822	2	Q2Q426_MACMU	Q2q426 macaca mula
39	137.5	5.8	1656	2	Q50SS7_ENTHI	Q50ss7 entamoeba h
40	137.5	5.8	4699	2	Q9V383_DROME	Q9v383 drosophila
41	136.5	5.7	966	2	Q22378_CAEEL	Q22378 caenorhabdi
42	136.5	5.7	2531	1	NOTC1_MOUSE	Q01705 mus musculu
43	135	5.7	919	2	Q61V24_CAEBR	Q61v24 caenorhabdi
44	134.5	5.6	635	2	Q7QP07_GIALA	Q7qp07 giardia lam
45	133.5	5.6	729	2	Q4RQK5_TETNG	Q4rqk5 tetraodon n

ALIGNMENTS

RESULT 1
Q9HDA5_HUMAN
ID Q9HDA5_HUMAN PRELIMINARY; PRT; 437 AA.
AC Q9HDA5;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Cell surface receptor (PRV1) (Polycythemia rubra vera 1).
GN Name=PRV1; ORFNames=UNQ595;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20218740; PubMed=10753836;
RA Temerinac S., Klippel S., Strunck E., Roder S., Lubbert M., Lange W.,
RA Azemar M., Meinhardt G., Schaefer H.E., Pahl H.L.;
RT "Cloning of PRV-1, a novel member of the uPAR receptor superfamily,
RT which is overexpressed in polycythemia rubra vera.";
RL Blood 95:2569-2576(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT vector.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
CC ---

CC ---
DR EMBL; AF146747; AAG00895.1; -; mRNA.
DR EMBL; AY358932; AAQ89291.1; -; mRNA.
DR EMBL; BT020111; AAV38914.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.

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DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 2.
KW   Receptor.
SQ   SEQUENCE   437 AA;  46363 MW;  3D40648723E43B65 CRC64;

  Query Match             100.0%;  Score 2381;  DB 2;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-176;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 2
Q8N6Q3_HUMAN
ID   Q8N6Q3_HUMAN   PRELIMINARY;   PRT;   437 AA.
AC   Q8N6Q3;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Polycythemia rubra vera 1.
GN   Name=PRV1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC029167; AAH29167.1; -; mRNA.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 2.
SQ   SEQUENCE   437 AA;  46419 MW;  CC4DE4EC1E7CFC4B CRC64;

  Query Match             99.5%;  Score 2370;  DB 2;  Length 437;
  Best Local Similarity   99.3%;  Pred. No. 4.2e-175;
  Matches  434;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSPVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLLDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGTTHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 3
Q96QH1_HUMAN
ID   Q96QH1_HUMAN   PRELIMINARY;   PRT;   437 AA.
AC   Q96QH1;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   NB1 Glycoprotein precursor.
GN   Name=NB1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21357611; PubMed=11465086;
RX   DOI=10.1002/1521-4141(200105)31:5<1301::AID-IMMU1301>3.0.CO;2-J;
RA   Kissel K., Santoso S., Hofmann C., Stroncek D., Bux J.;
RT   "Molecular basis of the neutrophil glycoprotein NB1 (CD177) involved
RT   in the pathogenesis of immunenneutropenia and transfusion reactions.";
RL   Eur. J. Immunol. 31:1301-1309(2001).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ290452; CAC44459.1; -; mRNA.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 2.
KW   Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22    437       NB1 protein.
SQ   SEQUENCE   437 AA;  46335 MW;  823D4F784986A42F CRC64;

  Query Match             99.1%;  Score 2360;  DB 2;  Length 437;
  Best Local Similarity   99.1%;  Pred. No. 2.5e-174;
  Matches  433;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSPVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPFW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDQQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSSLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 4
Q8R2S8_MOUSE
ID   Q8R2S8_MOUSE   PRELIMINARY;   PRT;   817 AA.
AC   Q8R2S8;
DT   01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2002, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   CD177 antigen.
GN   Name=Cd177;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RC   10 month old virgin mouse. Taken by biopsy.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RC   10 month old virgin mouse. Taken by biopsy.;
RG   NIH MGC Project;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC027283; AAH27283.1; -; mRNA.
DR   Ensembl; ENSMUSG00000052212; Mus musculus.
DR   MGI; MGI:1916141; 1190003K14Rik.
DR   MGI; MGI:1916141; Cd177.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 4.
SQ   SEQUENCE   817 AA;  87091 MW;  F22A8B073D6F7C60 CRC64;

  Query Match             49.5%;  Score 1179;  DB 2;  Length 817;
  Best Local Similarity   53.6%;  Pred. No. 1.7e-82;
  Matches  230;  Conservative   59;  Mismatches  122;  Indels   18;  Gaps    7;

Qy         19 VQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLIESGPQVSLVLSKGCTE 78
              : || || ||:: :  :| || |||      |: | ||||||||||:| ||:|||:||||
Db        397 LDALKCQHGTLKTIQDISKLPLQWTAGQKICNVGEGCQDTLMLIENGEQVNLVLTKGCTT 456

Qy         79 AKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPADPGSLRCPVCLS 138
              ||||| :||||| |||||: ||| |||::||||:|  : |||||  |   ||: |||:| |
Db        457 AKDQEAKVTEHRTGPGLSVTSYTRVCRKKDFCNDLSTTAPLWAPPPVTAPGTTRCPLCFS 516

Qy        139 MEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCNLLNGTQEIGPVG 198
              : | |   |::|| |:|||| |:| |||||| |:|:||||| |||||||||| ||||
Db        517 EQAC-ENAPEQVCPAGSTHCYSGVLSLRGGGIISDLKVQGCMSQPGCNLLNGTQTIGPVD 575

Qy        199 MTENC---NRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLLIDVGL 255
              ::| |   :    |:|:||          |:||  ||   :::|   ::|||||||||||
Db        576 VSERCSPPSETTELSCYRGVMFELGNGFAEEPVKWTAPGSQVCAPDEICQETLLLIDVGQ 635

Qy        256 TSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQ 315
              |  :|:|||| |||::   :| |  ||:|||||| |||| ||| | ||||||: ||
Db        636 KSAFLGSKGCSSPGAQDNIGVSIFSRLPGMLVASYTKFCSSHLCNGADSSSVLLSILPRP 695

Qy        316 AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQ 375
              | ||| ||| ||:  |:| | :  :|||||||||| | | | ||||:|::||||||:|
Db        696 DVPPPGDVQCPMCVELFGSCKS-TDSVTCPRGATHCYKGDIALQGGGLTTRVSIQGCMAP 754

Qy        376 PSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEG------LESLTWGVGL-ALAPAL 428
              |   ||  :: |||||| |  :      :||             |    | :|| ||  :|
Db        755 PIKPLLGDSKTIGIFSAEESSNY-----RHEDDVTSAPSLAWTLRLSAWMLGLSALLSSL 809

Qy        429 WWGVVCPSC 437
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              : | :|| |
Db        810 YAG-ICPLC 817


RESULT 5
Q711Q2_HUMAN
ID   Q711Q2_HUMAN   PRELIMINARY;   PRT;   248 AA.
AC   Q711Q2;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   NB1 glycoprotein precursor.
GN   Name=NB1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kissel K., Scheffler S., Bux J.;
RT   "mRNA of NB1 (HNA-2a) negative indviduals.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Bux J., Scheffler S., Kissel K.;
RT   "Molecular basis of the NB1 (HNA-2a)-negative phenotype.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ310433; CAC83724.1; -; mRNA.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
KW   Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22    248       NB1 glycoprotein negative phenotype #1.
SQ   SEQUENCE   248 AA;  27165 MW;  E385D3DB37C515E1 CRC64;

  Query Match             46.5%;  Score 1108;  DB 2;  Length 248;
  Best Local Similarity   97.1%;  Pred. No. 1.3e-77;
  Matches  203;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSPVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEYRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFL 209
              ||| |||||||| |||||||||: ||||
Db        181 PQPVCNLLNGTQEFGPVGMTENCDMKDFL 209


RESULT 6
Q8NCV9_HUMAN
ID   Q8NCV9_HUMAN   PRELIMINARY;   PRT;   145 AA.
AC   Q8NCV9;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Glycoprotein NB1 precursor.
GN   Name=NB1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22006006; PubMed=12010833; DOI=10.1182/blood.V99.11.4231;
RA   Kissel K., Scheffler S., Kerowgan M., Bux J.;
RT   "Molecular basis of NB1 (HNA-2a, CD177) deficiency.";
RL   Blood 99:4231-4233(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ305326; CAC83758.1; -; mRNA.
DR   LinkHub; Q8NCV9; -.
KW   Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22    145       glycoprotein NB1.
SQ   SEQUENCE   145 AA;  15709 MW;  EF7FB498A8B39053 CRC64;

  Query Match             28.9%;  Score 687;  DB 2;  Length 145;
  Best Local Similarity   90.3%;  Pred. No. 3e-45;
  Matches  131;  Conservative    0;  Mismatches    4;  Indels   10;  Gaps    1;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSPVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEG 145
              ||||||||           | |  ||
Db        121 APQPPADP----------MMGAAEG 135


RESULT 7
Q9D0T8_MOUSE
ID   Q9D0T8_MOUSE   PRELIMINARY;   PRT;   212 AA.
AC   Q9D0T8;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   22-NOV-2005, sequence version 2.
DT   07-FEB-2006, entry version 24.
DE   18-day embryo whole body cDNA, RIKEN full-length enriched library,
DE   clone:1190003K14 product:hypothetical protein, full insert sequence.
DE   (Fragment).
GN   Name=Cd177;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
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RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AK004472; BAB23319.2; -; mRNA.
DR MGI; MGI:1916141; Cd177.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 212 AA; 22172 MW; 0C4B2B2A17086C4E CRC64;

Query Match 22.0%; Score 523; DB 2; Length 212;
Best Local Similarity 50.2%; Pred. No. 2.4e-32;
Matches 110; Conservative 29; Mismatches 66; Indels 14; Gaps 5;

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Qy        226 EPTDWTTSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGV 285
              ||  ||   :::|   ::|||||||||||  |  :|:||||: |||::   :| |  ||:
Db          1 EPVKWTAPGSQVCAPDEICQETLLLIDVGQKSAFLGSKGCSSPGAQDNIGVSIFSRLPGM 60

Qy        286 LVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCP 345
              |||||| |||| ||| | ||||||: ||    | ||| ||| ||:  |:| | :  :|||
Db         61 LVASYTKFCSSHLCNGADSSSVLLSILPRPDVPPPGDVQCPMCVELFGSCKS-TDSVTCP 119

Qy        346 RGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQH 405
              ||||||| | | | ||||:|::||||||:| |   ||  :: |||||| |  :      :|
Db        120 RGATHCYKGDIALQGGGLTTRVSIQGCMAPPIKPLLGDSKTIGIFSAEESSNY-----RH 174

Qy        406 EGGGAEG------LESLTWGVGL-ALAPALWWGVVCPSC 437
              |            |    | :|| ||  :|: | :|| |
Db        175 EDDVTSAPSLAWTLRLSAWMLGLSALLSSLYAG-ICPLC 212


RESULT 8
Q810N3_MOUSE
ID   Q810N3_MOUSE   PRELIMINARY;   PRT;   246 AA.
AC   Q810N3;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Hypothetical protein BC049730.
GN   Name=BC049730;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Director MGC Project;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC049730; AAH49730.1; -; mRNA.
DR   Ensembl; ENSMUSG00000045587; Mus musculus.
DR   MGI; MGI:2681843; BC049730.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   246 AA;  26554 MW;  0874C995EEC94E06 CRC64;

  Query Match             15.9%;  Score 378.5;  DB 2;  Length 246;
  Best Local Similarity   37.8%;  Pred. No. 4.5e-21;
  Matches   90;  Conservative   37;  Mismatches   96;  Indels   15;  Gaps    6;

Qy        203 CNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCE--VGQVCQETLLLIDVGLTSTLV 260
              |   | | |  |: :    | ::   :|  : |   |   |::|||  ||||||  | ::
Db         18 CPCSDTLNCQEGSVMKFGQNFSRTSIEWIVNQTVGSEKNKGEMCQEIFLLIDVGEKSLIL 77

Qy        261 GTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVP 320
              |||| :||  :  :|| : |  ||:: ||| ||| :||||:|||: |||: |       |
Db         78 GTKGITTVPGKR-KKTDVFSPGPGIVSASYVHFCDTDLCNNASSTKVLLDLLKLSEYNEP 136

Qy        321 GDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFL 380
              |  :|| |:   |:|:: |    ||:  | ||   : : || ||   || ||:    ::|
Db        137 GTTKCPVCLDFKGSCNTESNHTLCPKD-TKCYAASLGVHGGDLSAIFSISGCLNSSHTYL 195

Qy        381 LNHTRQIGIFSAREKRDVQPPASQHEGGGAEGL----ESLTWGVGLALAPALWWGVVC 434
              ||:   ||| | :|  :     |      ::||      |||  || ||  |   |:|
Db        196 LNNQNTIGIISIKETLESNVTLS------SQGLLVPSILLTWMFGL-LALCLQRSVLC 246


RESULT 9
Q78KC5_MOUSE
ID   Q78KC5_MOUSE   PRELIMINARY;   PRT;   153 AA.
AC   Q78KC5;
DT   22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   22-NOV-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Cd177 protein.
GN   Name=Cd177;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RG   NIH MGC Project;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC005615; AAH05615.1; -; mRNA.
DR   MGI; MGI:1916141; Cd177.
SQ   SEQUENCE   153 AA;  16087 MW;  6DEAAF297B4FC579 CRC64;

  Query Match             15.4%;  Score 366;  DB 2;  Length 153;
  Best Local Similarity   50.6%;  Pred. No. 2.4e-20;
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  Matches   81;  Conservative   18;  Mismatches   47;  Indels   14;  Gaps    5;

Qy        285 VLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTC 344
              :|||||| |||| ||| | |||||| : ||    | ||| ||| ||:  |:| | :  :||
Db          1 MLVASYTKFCSSHLCNGADSSSVLLSILPRPDVPPPGDVQCPMCVELFGSCKS-TDSVTC 59

Qy        345 PRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQ 404
              |||||||| | | |||:|::|||||:| |   ||  :: |||||| |  :     :
Db         60 PRGATHCYKGDIALQGGGLTTRVSIQGCMAPPIKPLLGDSKTIGIFSAEESSNY-----R 114

Qy        405 HEGGGAEG------LESLTWGVGL-ALAPALWWGVVCPSC 437
              ||            |    | :|| ||  :|: | :|| |
Db        115 HEDDVTSAPSLAWTLRLSAWMLGLSALLSSLYAG-ICPLC 153


RESULT 10
Q9BPY7_HUMAN
ID   Q9BPY7_HUMAN   PRELIMINARY;   PRT;   249 AA.
AC   Q9BPY7;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Putative cell surface receptor NYD-SP8 (GTPR867) (Scleroderma-
DE   associated autoantigen).
GN   ORFNames=UNQ867;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Li J.M., Zhou Z.M., Sha J.H., Lin M., Wang L.R., Zhou Y.D., Zhu H.H.,
RA   Zhu H.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Yang J., Xie Y., Ni Z., Wang Z., Zhong L., Lei H., Hu l.L., Shi L.,
RA   Zhao G., Kong X.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY014285; AAK27310.1; -; mRNA.
DR   EMBL; AY359077; AAQ89436.1; -; mRNA.
DR   EMBL; AF353396; AAK38662.1; -; mRNA.
DR   Ensembl; ENSG00000131126; Homo sapiens.
DR   LinkHub; Q9BPY7; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
KW   Receptor.
SQ   SEQUENCE   249 AA;  26667 MW;  CEDC82D7C4F04821 CRC64;

  Query Match           14.3%;  Score 341.5;  DB 2;  Length 249;
  Best Local Similarity   34.2%;  Pred. No. 3.3e-18;
  Matches   76;  Conservative   38;  Mismatches   93;  Indels   15;  Gaps    7;

Qy        209 LTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTV 268
              | | :| ::    : |    :|||   | |: | :||||:|:|  |  : :: ||||
Db         26 LYCQKGLSMTVEADPA-NMFNWTTEEVETCDKGALCQETILIIKAGTETAILATKGCIPE 84

Qy        269 GAQNSQKTTI--HSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCP 326
              |    :  ||  ||:|||::| ||:::|    ||   | |          |: |     ||
Db         85 G---EEAITIVQHSSPPGLIVTSYSNYCEDSFCNDKDSLSQFWEFSETTASTVSTTLHCP 141

Qy        327 TCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQ 386
              |||  |||| | :| : || | | || | : ::|||: : : ::|| |      |::
Db        142 TCV-ALGTCFS-APSLPCPNGTTRCYQGKLEITGGGIESSVEVKGCTAMIGCRLMSGILA 199

Qy        387 IGIFSARE----KRDVQPPASQHEGGGAEGLESLTWGVGLAL 424
              :|    ||    :   ||  :::   ||  |    ||: | |
Db        200 VGPMFVREACPHQLLTQPRKTEN---GATCLPIPVWGLQLLL 238


RESULT 11
Q7L5R2_HUMAN
ID   Q7L5R2_HUMAN   PRELIMINARY;   PRT;   267 AA.
AC   Q7L5R2;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Testis expressed sequence 101.
GN   Name=TEX101;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Director MGC Project;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC001861; AAH01861.2; -; mRNA.
DR   Ensembl; ENSG00000131126; Homo sapiens.
DR   HGNC; HGNC:30722; TEX101.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
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SQ   SEQUENCE   267 AA;  28532 MW;  59CAF4951E2AB760 CRC64;

  Query Match             14.3%;  Score 341.5;  DB 2;  Length 267;
  Best Local Similarity   34.2%;  Pred. No. 3.6e-18;
  Matches   76;  Conservative   38;  Mismatches   93;  Indels   15;  Gaps    7;

Qy        209 LTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTV 268
              | | :| ::    : |    :|||   | |: | :||||:|:|   |  : :: ||||
Db         44 LYCQKGLSMTVEADPA-NMFNWTTEEVETCDKGALCQETILIIKAGTETAILATKGCIPE 102

Qy        269 GAQNSQKTTI--HSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCP 326
              |    :  ||  ||:|||::| ||:::|    ||   | |          |: |     ||
Db        103 G---EEAITIVQHSSPPGLIVTSYSNYCEDSFCNDKDSLSQFWEFSETTASTVSTTLHCP 159

Qy        327 TCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQ 386
              ||| |||| | :| : || | | || | : ::|||: : : ::|| |      |::
Db        160 TCV-ALGTCFS-APSLPCPNGTTRCYQGKLEITGGGIESSVEVKGCTAMIGCRLMSGILA 217

Qy        387 IGIFSARE----KRDVQPPASQHEGGGAEGLESLTWGVGLAL 424
              :|    ||    :   ||  :::   ||  |    ||: | |
Db        218 VGPMFVREACPHQLLTQPRKTEN---GATCLPIPVWGLQLLL 256


RESULT 12
Q9BY14_HUMAN
ID   Q9BY14_HUMAN   PRELIMINARY;   PRT;   267 AA.
AC   Q9BY14;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scleroderma-associated autoantigen.
GN   Name=TEX101;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yang J., Ni Z., Xie Y., Zhong L., Lei H., Shi L., Zhao G., Hu L.,
RA   Kong X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF241268; AAK28327.1; -; mRNA.
DR   Ensembl; ENSG00000131126; Homo sapiens.
DR   LinkHub; Q9BY14; -.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
SQ   SEQUENCE   267 AA;  28617 MW;  30D15F7BCA40ACC5 CRC64;

  Query Match             13.9%;  Score 330.5;  DB 2;  Length 267;
  Best Local Similarity   33.8%;  Pred. No. 2.6e-17;
  Matches   75;  Conservative   38;  Mismatches   94;  Indels   15;  Gaps    7;

Qy        209 LTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTV 268
              | | :| ::    : |    :|||   | |: | :||||:|:|   |  : :: ||||
Db         44 LYCQKGLSMTVEADPA-NMFNWTTEEVETCDKGALCQETILIIKAGTETAILATKGCIPE 102

Qy        269 GAQNSQKTTI--HSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCP 326
              |    :  ||  ||:|||::| ||:::|    ||   | |          |: |     ||
Db        103 G---EEAITIVQHSSPPGLIVTSYSNYCEDSFCNDKDSLSQFWEFSETTASTVSTTLHCP 159

Qy        327 TCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQ 386
              ||| |||| | :| : || | | || | : ::|||: : : ::|| |      |::
Db        160 TCV-ALGTCFS-APSLPYPNGTTRCYQGKLEITGGGIESSVEVKGCTAMIGCRLMSGILA 217

Qy        387 IGIFSARE----KRDVQPPASQHEGGGAEGLESLTWGVGLAL 424
              :|    ||    :   ||  :::   ||  |    ||: | |
Db        218 VGPMFVREACPHQLLTQPRKTEN---GATCLPIPVWGLQLLL 256


RESULT 13
Q924B5_RAT
ID   Q924B5_RAT     PRELIMINARY;   PRT;   250 AA.
AC   Q924B5;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Glycoprotein TEC-21.
GN   Name=Tex101;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Wistar;
RX   MEDLINE=21542636; PubMed=11686435;
RA   Halova I., Draberova L., Draber P.;
RT   "New monoclonal antibodies to rat testicular antigen, TEC-21.";
RL   Folia Biol. (Praha) 47:180-182(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Wistar;
RX   MEDLINE=21668242; PubMed=11809740; DOI=10.1093/intimm/14.2.213;
RA   Halova I., Draberova L., Draber P.;
RT   "A novel lipid raft-associated glycoprotein, TEC-21, activates rat
RT   basophilic leukemia cells independently of the type 1 Fc epsilon
RT   receptor.";
RL   Int. Immunol. 14:213-223(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF347056; AAK58911.1; -; mRNA.
DR   Ensembl; ENSRNOG00000020057; Rattus norvegicus.
DR   RGD; 621373; Tex101.
DR   GO; GO:0045121; C:lipid raft; IMP.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
SQ   SEQUENCE   250 AA;  27004 MW;  CFF31D13C980AC4C CRC64;

  Query Match             12.5%;  Score 298.5;  DB 2;  Length 250;
  Best Local Similarity   30.9%;  Pred. No. 7.2e-15;
  Matches   71;  Conservative   41;  Mismatches   95;  Indels   23;  Gaps    8;

Qy         19 VQALLCQFGTVQHVWKVSDLPR---QWTPKNTSCDSGLGCQDTLMLIES-GPQVSLVLSK 74
              || : |:   |     : | |     || |   |: |  ||:|::||:: | : ::: ||
Db         23 VQNIYCE---VSRTLSLEDNPSGTFNWTSKAEKCNPGEFCQETVLLIKAEGTKTAILASK 79

Qy         75 GCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVN-SLPLWAPQPPAD---PGS 130
                 |     :    ::  |||  |||:  |  :  |||  | :  | ||:| |     |:
Db         80 SCVPQGAETMTFVQYTAPPGLVAISYSNYC-NDSLCNNRNNLASILQAPEPTATSNMSGA 138

Qy        131 LRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCNLLNG 190
               || ||::| |    :   |  ||| || | : | |||: | : |:||    || |:
Db        139 RHCPTCLALEPCSSAPSMP-CANGTTQCYHGKIELSGGGMDSVVHVKGCTTAIGCRLMAK 197

Qy        191 TQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
               : :||: : | |: : ||          |  :|:    |  ::  : |:
Db        198 MESVGPMTVKETCSYQSFL----------HPRMAEIGASWMPTSLWVLEL 237


RESULT 14
Q8CFJ5_MOUSE
ID   Q8CFJ5_MOUSE   PRELIMINARY;   PRT;   196 AA.
AC   Q8CFJ5;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Hypothetical protein MGC48079.
GN   Name=MGC48079;
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OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus gland;
RA   Strausberg R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC037749; AAH37749.1; -; mRNA.
DR   Ensembl; ENSMUSG00000058717; Mus musculus.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   196 AA;  20969 MW;  3575C7D733237486 CRC64;

  Query Match             12.3%;  Score 294;  DB 2;  Length 196;
  Best Local Similarity   36.3%;  Pred. No. 1.2e-14;
  Matches   66;  Conservative   32;  Mismatches   78;  Indels    6;  Gaps    4;

Qy        257 STLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQA 316
              | :: :|| |   :::    : |  ||:: ||| |||:::|||||:|:|||: ::
Db         20 SLILASKGSSKAESKSVNDVQVFSGGPGIVTASYVHFCNTELCNSANSTSVLIKNVKLSE 79

Qy        317 APVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQP 376
              :   |  ||| |:   |:||  :  : ||:  | ||   : : ||||    |: ||:|
Db         80 SSGQGSIQCPVCLHFRGSCSQHTKFVLCPKD-TRCYFSDMTVEGGGLKNFFSLDGCLANS 138

Qy        377 SSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGL-ALAPALWWGVVCP 435
              :  ||     ||||  |   |  | |             ||| :|| ||  :|: | :||
Db        139 AKNLLKSQTSIGIFSVVE---VSNPGSSKSPSRVVASILLTWMLGLRALLSSLYAG-ICP 194

Qy        436 SC 437
              ||
Db        195 LC 196


RESULT 15
Q7TQN2_CRIGR
ID   Q7TQN2_CRIGR   PRELIMINARY;   PRT;   253 AA.
AC   Q7TQN2;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Lipid raft-associated glycoprotein TEC-21.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Charvatova L., Tumova M., Draber P.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY309070; AAP73441.1; -; mRNA.
DR   InterPro; IPR001526; LY6_UPAR.
DR   Pfam; PF00021; UPAR_LY6; 1.
SQ   SEQUENCE   253 AA;  26978 MW;  A1BB49698B2589A7 CRC64;

  Query Match             12.3%;  Score 293;  DB 2;  Length 253;
  Best Local Similarity   32.5%;  Pred. No. 1.9e-14;
  Matches   78;  Conservative   41;  Mismatches   83;  Indels   38;  Gaps   12;

Qy        218 MTHGNLAQ-------------EPT---DWTT--SNTEMCEVGQVCQETLLLIDV-GLTS 257
              ::|  |||               :|:   :||:     | |  |::||||:|||   |  :
Db         16 VSHQTLAQSLQCAVSKVLRLEDDPSRTFNWTSKPDKVETCNPGELCQETVLLIKAEGTKT 75

Qy        258 TLVGTKGCSTVGAQNSQKTTI--HSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQ 315
               :| :|||:   ::  :  |   :: ||||:  ||:::|:| |||  :| :| |   ||
Db         76 AVVASKGCA---SREIEAVTFIQYTPPPGVIAISYSNYCNSSLCN--NSKNVSLFWKPPD 130

Qy        316 ---AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC 372
                 : : |   |||||  ||:||| :| | |    | || | | |||||: : : |:||
Db        131 TTATSKILGALSCPTCV-ALGSCSS-APSMPCANSTTQCYQGKIELSGGGMDSVLHIKGC 188

Qy        373 VAQPSSFLLNHTRQIGIFSAREKRD----VQPPASQHEGGGAEGLESLTWGVGLALAPAL 428
                       |:     :|  : :|       :||   : |   | |  :  | : | |   |
Db        189 TTAIGCRLMAAITSVGPMTVKETCSYHSLLQP--RKAEESRASGRSTSLWVLELLLPAVL 246


Search completed: July 11, 2006, 09:29:54
Job time : 303 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:21:17 ; Search time 195 Seconds
(without alignments)
1024.634 Million cell updates/sec

Title: US-10-727-619-2
Perfect score: 2381
Sequence: 1 MSAVLLLALLGFILPLPGVQ.....WGVGLALAPALWWGVVCPSC 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2381	100.0	437	3	AAY87750	Aay87750 Human PRV
2	2381	100.0	437	3	AAY66737	Aay66737 Membrane-
3	2381	100.0	437	3	AAY96733	Aay96733 PRO1863,
4	2381	100.0	437	4	AAU12404	Aau12404 Human PRO
5	2381	100.0	437	4	AAB70851	Aab70851 Human PRV
6	2381	100.0	437	4	AAB65260	Aab65260 Human PRO
7	2381	100.0	437	5	AAU83672	Aau83672 Human PRO
8	2381	100.0	437	5	ABG92707	Abg92707 Human sec
9	2381	100.0	437	5	ABG91359	Abg91359 Novel hum
10	2381	100.0	437	5	ABG31399	Abg31399 Human PRO
11	2381	100.0	437	5	ADY31902	Ady31902 Novel hum
12	2381	100.0	437	6	ABU72375	Abu72375 Novel hum
13	2381	100.0	437	6	ABU58075	Abu58075 Human PRO
14	2381	100.0	437	6	ABU59153	Abu59153 Novel hum
15	2381	100.0	437	6	ABU80865	Abu80865 Human sec
16	2381	100.0	437	6	ABU82665	Abu82665 Human sec
17	2381	100.0	437	6	ABO17848	Abo17848 Novel hum
18	2381	100.0	437	6	ABU60584	Abu60584 Human sec
19	2381	100.0	437	6	ABU80819	Abu80819 Human PRO
20	2381	100.0	437	6	ABO33785	Abo33785 Novel hum
21	2381	100.0	437	6	ABU13966	Abu13966 Human PRO
22	2381	100.0	437	6	ABU81102	Abu81102 Human PRO
23	2381	100.0	437	6	ABU72551	Abu72551 Novel hum
24	2381	100.0	437	6	ABU66802	Abu66802 Human PRO
25	2381	100.0	437	6	ABG73312	Abg73312 Human PRO
26	2381	100.0	437	6	ABU59883	Abu59883 Novel sec
27	2381	100.0	437	6	ABU59300	Abu59300 Human sec
28	2381	100.0	437	6	ABO25997	Abo25997 Human PRO
29	2381	100.0	437	6	ABO25073	Abo25073 Human sec
30	2381	100.0	437	6	ABU82128	Abu82128 Novel hum
31	2381	100.0	437	6	ABU59006	Abu59006 Human sec
32	2381	100.0	437	6	ABU60811	Abu60811 Human sec
33	2381	100.0	437	6	ABU92384	Abu92384 Novel hum
34	2381	100.0	437	6	ABU59449	Abu59449 Novel hum
35	2381	100.0	437	6	ABU67078	Abu67078 Human sec
36	2381	100.0	437	6	ABU81234	Abu81234 Human PRO
37	2381	100.0	437	6	ABU92215	Abu92215 Novel hum
38	2381	100.0	437	6	ABU10921	Abu10921 Human PRO
39	2381	100.0	437	6	ABU81673	Abu81673 Novel hum
40	2381	100.0	437	6	ABU88612	Abu88612 Human sec
41	2381	100.0	437	6	ABO34126	Abo34126 Human PRO
42	2381	100.0	437	6	ADA45985	Ada45985 Novel hum
43	2381	100.0	437	6	ADA76416	Ada76416 Human PRO
44	2381	100.0	437	6	ABJ72308	Abj72308 Human PRO
45	2381	100.0	437	6	ADA19066	Ada19066 Human PRO

ALIGNMENTS

RESULT 1
AAY87750
ID AAY87750 standard; protein; 437 AA.
XX
AC AAY87750;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human PRV-1 protein.
XX
KW PRV-1; human; polycythaemia rubra vera; PRV; antiproliferative;
KW treatment; detection; diagnosis.
XX
OS Homo sapiens.
XX
PN DE19849044-A1.
XX
PD 27-APR-2000.
XX
PF 23-OCT-1998; 98DE-01049044.
XX
PR 23-OCT-1998; 98DE-01049044.
XX
PA (UYFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
XX
PI Pahl H, Temerinac S;
XX
DR WPI; 2000-319347/28.
DR N-PSDB; AAA12386.
XX
PT New polycythemia rubra vera-related polypeptide useful for diagnosis and
PT for developing therapeutic antibodies.
XX
PS Claim 6; Fig 2; 6pp; German.
XX
CC This invention describes a novel PRV-1 protein (I) detected in humans
CC suffering from the condition polycythaemia rubra vera (PRV). The product
CC of the invention has antiproliferative activity. The encoding nucleic
CC acid sequence is used to express recombinant PRV-1 polypeptides and as a
CC source of antisense sequences that can be expressed in vivo for treatment
CC of PRV. (I) is used to raise specific mono or polyclonal antibodies and
CC these are used to diagnose PRV (by detecting (I), or its epitopes, in
CC immunoassays) or for treatment of PRV (optionally when coupled to a
CC cytotoxin). This sequence represents the human PRV-1 protein described in
CC the method of the invention
XX

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SQ   Sequence 437 AA;

  Query Match             100.0%;  Score 2381;  DB 3;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
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Db        421 GLALAPALWWGVVCPSC 437


RESULT 2
AAY66737
ID   AAY66737 standard; protein; 437 AA.
XX
AC   AAY66737;
XX
DT   05-APR-2000  (first entry)
XX
DE   Membrane-bound protein PRO1181.
XX
KW   Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW   pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO9963088-A2.
XX
PD   09-DEC-1999.
XX
PF   02-JUN-1999;   99WO-US012252.
XX
PR   02-JUN-1998;   98US-0087607P.
PR   02-JUN-1998;   98US-0087609P.
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PR   03-JUN-1998;   98US-0087827P.
PR   04-JUN-1998;   98US-0088021P.
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PR   04-JUN-1998;   98US-0088028P.
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PR   04-JUN-1998;   98US-0088030P.
PR   04-JUN-1998;   98US-0088033P.
PR   04-JUN-1998;   98US-0088326P.
PR   05-JUN-1998;   98US-0088167P.
PR   05-JUN-1998;   98US-0088202P.
PR   05-JUN-1998;   98US-0088212P.
PR   05-JUN-1998;   98US-0088217P.
PR   09-JUN-1998;   98US-0088655P.
PR   10-JUN-1998;   98US-0088722P.
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PR   01-JUL-1998;   98US-0091358P.
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PR   17-AUG-1998;   98US-0096895P.
PR   17-AUG-1998;   98US-0096897P.
PR   18-AUG-1998;   98US-0096949P.
PR   18-AUG-1998;   98US-0096950P.
PR   18-AUG-1998;   98US-0096959P.
PR   18-AUG-1998;   98US-0096960P.
PR   18-AUG-1998;   98US-0097022P.
PR   19-AUG-1998;   98US-0097141P.
PR   20-AUG-1998;   98US-0097218P.
PR   24-AUG-1998;   98US-0097661P.
PR   26-AUG-1998;   98US-0097951P.
PR   26-AUG-1998;   98US-0097952P.
PR   26-AUG-1998;   98US-0097954P.
PR   26-AUG-1998;   98US-0097955P.
PR   26-AUG-1998;   98US-0097971P.
PR   26-AUG-1998;   98US-0097974P.
PR   26-AUG-1998;   98US-0097978P.
PR   26-AUG-1998;   98US-0097979P.
PR   26-AUG-1998;   98US-0097986P.
PR   26-AUG-1998;   98US-0098014P.
PR   31-AUG-1998;   98US-0098525P.
PR   16-SEP-1998;   98US-0100634P.
PR   12-JAN-1999;   99US-0115565P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Chen J,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK;
PI   Wood WI,  Yuan J;
XX
DR   WPI; 2000-072883/06.
DR   N-PSDB; AAZ65083.
XX
PT   Membrane-bound proteins and related nucleotide sequences.
XX
PS   Claim 12; Fig 250; 822pp; English.
XX
CC   The invention provides membrane-bound PRO polypeptides and
CC   polynucleotides encoding them. The PRO sequences of the invention were
CC   identified based on extracellular domain homology screening. The PRO
CC   sequences have homology with proteins including LDL receptors, TIE
CC   ligands and various enzymes. The membrane-bound proteins and receptor
CC   molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC   immunoadhesins, for instance, can be used as therapeutic agents to block
CC   receptor-ligand interactions. The membrane-bound proteins can also be
CC   employed for screening of potential peptide or small molecule inhibitors
CC   of the relevant receptor/ligand interaction. The PRO encoding sequences
CC   are useful as hybridization probes, in chromosome and gene mapping and in
CC   the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC   also be useful for the preparation of PRO polypeptides, especially by
CC   recombinant techniques
XX
SQ   Sequence 437 AA;

  Query Match             100.0%;  Score 2381;  DB 3;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 3
AAY96733
ID   AAY96733 standard; protein; 437 AA.
XX
AC   AAY96733;
XX
DT   26-SEP-2000  (first entry)
XX
DE   PRO1863, a novel transmembrane protein.
XX
KW   PRO1863; secreted protein; transmembrane protein; recombinant production;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .15
FT                   /label= Signal_peptide
FT   Modified-site   46. .49
FT                   /note= "N-glycosylation site"
FT   Modified-site   51. .54
FT                   /note= "Glycosaminoglycan attachment site"
FT   Modified-site   54. .59
FT                   /note= "N-myristoylation site"
FT   Modified-site   75. .80
FT                   /note= "N-myristoylation site"
FT   Modified-site   141. .146
FT                   /note= "N-myristoylation site"
FT   Modified-site   154. .159
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FT                   /note= "N-myristoylation site"
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FT                   /note= "N-myristoylation site"
FT   Modified-site   169. .174
FT                   /note= "N-myristoylation site"
FT   Modified-site   189. .192
FT                   /note= "N-glycosylation site"
FT   Modified-site   198. .203
FT                   /note= "N-myristoylation site"
FT   Domain          243. .260
FT                   /label= Transmembrane_domain
FT   Modified-site   254. .259
FT                   /note= "N-myristoylation site"
FT   Modified-site   261. .266
FT                   /note= "N-myristoylation site"
FT   Modified-site   269. .274
FT                   /note= "N-myristoylation site"
FT   Modified-site   284. .289
FT                   /note= "N-myristoylation site"
FT   Modified-site   333. .338
FT                   /note= "N-myristoylation site"
FT   Modified-site   347. .352
FT                   /note= "N-myristoylation site"
FT   Modified-site   359. .362
FT                   /note= "Glycosaminoglycan attachment site"
FT   Modified-site   360. .365
FT                   /note= "N-myristoylation site"
FT   Modified-site   361. .366
FT                   /note= "N-myristoylation site"
FT   Modified-site   382. .385
FT                   /note= "N-glycosylation site"
FT   Modified-site   388. .393
FT                   /note= "N-myristoylation site"
FT   Modified-site   408. .413
FT                   /note= "N-myristoylation site"
FT   Modified-site   419. .424
FT                   /note= "N-myristoylation site"
XX
PN   WO200036102-A2.
XX
PD   22-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US028634.
XX
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2000-431586/37.
DR   N-PSDB; AAA51263.
XX
PT   Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT   transmembrane polypeptide.
XX
PS   Claim 12; Fig 10; 154pp; English.
XX
CC   This is PRO1863, a novel transmembrane protein. The invention concerns
CC   novel secreted and transmembrane proteins, designated PRO polypeptides.
CC   The cDNA and gene sequences are useful in the recombinant production of
CC   PRO polypeptides, as a hybridization probe to screen libraries to isolate
CC   cDNAs with sequence identity to PRO polypeptides or to map the gene
CC   encoding the PRO polypeptides and analyzing genetic disorders. The
CC   cDNA/gene can also be used to produce transgenic animals useful for the
CC   development and screening of therapeutically useful reagents. They can
CC   also be used in gene therapy, e.g. to replace a defective gene
XX
SQ   Sequence 437 AA;

  Query Match             100.0%;  Score 2381;  DB 3;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 4
AAU12404
ID   AAU12404 standard; protein; 437 AA.
XX
AC   AAU12404;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO1181 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
```

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PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21476.
XX
PT   Isolated , secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT   polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT   breast, prostate, cervical.
XX
PS   Claim 12; Fig 466; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC   polypeptides. The PRO polypeptides are useful to detect other PRO
CC   polypeptides, to link bioactive molecules to cells expressing PRO
CC   polypeptides, to modulate biological activities of cells expressing PRO
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 437 AA;
```

```
  Query Match           100.0%;  Score 2381;  DB 4;  Length 437;
  Best Local Similarity  100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437
```

```
RESULT 5
AAB70851
ID   AAB70851 standard; protein; 437 AA.
XX
AC   AAB70851;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Human PRV-1 protein.
XX
KW   PRV-1; human; hemostatic; polycythemia rubra vera; antisense therapy;
KW   treatment; diagnosis; pancytopenia; bone-marrow; blood; growth factor;
KW   pancytopathy; hematopoietic system disorder.
XX
OS   Homo sapiens.
XX
PN   DE19947010-A1.
XX
PD   05-APR-2001.
XX
PF   30-SEP-1999;   99DE-01047010.
XX
PR   30-SEP-1999;   99DE-01047010.
XX
PA   (UYFR-) UNIV FREIBURG.
XX
PI   Pahl H;
XX
DR   WPI; 2001-246167/26.
DR   N-PSDB; AAF61560.
XX
PT   New cloned PRV-1 gene associated with polycythemia rubra vera, e.g.
PT   useful for preparing antisense molecules or polypeptides for treatment or
PT   diagnosis of disorders of the hematopoietic system.
XX
```

PS Claim 3; Fig 2; 10pp; German.
XX
CC This invention describes a novel cloned PRV-1 gene (I) which has
CC hemostatic activity and is associated with polycythemia rubra vera (PRV).
CC (I) is useful for: (1) producing a recombinant PRV-1 polypeptide; (2)
CC producing antisense molecules useful for diagnosis and treatment of PRV;
CC (3) preparing medicaments for treating pancytopenias and pancytopathies
CC of the bone-marrow and blood. The polypeptide is useful: (1) as a growth
CC factor for inducing hematopoietic stem cells to form erythroid colonies;
CC (2) for preparing medicaments for treating pancytopenias and
CC pancytopathies of the bone-marrow and blood; (3) for treating and/or
CC multiplying autologous cells and/or established cell lines ex vivo or in
CC vitro; and (4) for producing antibodies useful for diagnosis of PRV or
CC other disorders of the hematopoietic system. This sequence represents the
CC human PRV-1 protein described in the invention
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437
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RESULT 6
AAB65260
ID AAB65260 standard; protein; 437 AA.
XX
AC AAB65260;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1181 (UNQ595) protein sequence SEQ ID NO:355.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44229.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 250; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy       121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy       181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy       241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy       301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy       361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy       421 GLALAPALWWGVVCPSC 437
             |||||||||||||||||
Db       421 GLALAPALWWGVVCPSC 437
```

RESULT 7
AAU83672
ID AAU83672 standard; protein; 437 AA.
XX
AC AAU83672;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 162.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR N-PSDB; ABK33616.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
PS Claim 11; Fig 162; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy        61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy       121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy       181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy       241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy       301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy       361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy       421 GLALAPALWWGVVCPSC 437
             |||||||||||||||||
Db       421 GLALAPALWWGVVCPSC 437
```

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RESULT 8
ABG92707
ID   ABG92707 standard; protein; 437 AA.
XX
AC   ABG92707;
XX
DT   18-NOV-2002  (first entry)
XX
DE   Human secreted protein PRO1863.
XX
KW   Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
KW   PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW   inflammatory disorder; immune related disease; rheumatoid arthritis;
KW   systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW   autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW   psoriasis; allergic disease of the lung; graft-versus host disease;
KW   tumour; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002098506-A1.
XX
PD   25-JUL-2002.
XX
PF   27-DEC-2001; 2001US-00033301.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-690475/74.
DR   N-PSDB; ABS68390.
XX
PT   Novel secreted and transmembrane polypeptides and polynucleotides useful
PT   for diagnosis and treatment of inflammatory disorders and immune-related
PT   diseases, and identifying modulators.
XX
PS   Claim 12; Fig 10; 125pp; English.
XX
CC   The invention relates to an isolated polypeptide having at least 80%
CC   amino acid sequence identity to secreted and transmembrane polypeptides
CC   PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
CC   PRO1927 and their encoding nucleic acids. Also included are vectors, host
CC   cells and antibodies against PRO polypeptides. PRO proteins are useful
CC   for identifying modulators of the polypeptide. PRO1868 useful for the
CC   diagnosis and treatment of inflammatory and immune related diseases
CC   including systemic lupus erythematosus, rheumatoid arthritis, systemic
CC   sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
CC   infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
CC   versus host disease and tumours. Pro nucleic acids are useful for
CC   constructing hybridisation probes for mapping the gene that encodes that
CC   PRO and for the genetic analysis of individuals with genetic disorders,
CC   and for generating transgenic animals which are useful in the development
CC   and screening of therapeutically useful reagents. PRO nucleic acids are
CC   also useful for gene therapy, chromosome identification, and tissue
CC   typing. PRO proteins are useful as molecular weight markers for protein
CC   electrophoresis purposes. The anti-PRO antibodies are useful in
CC   diagnostic assays for PRO, e.g. detecting its expression in specific
CC   cells, tissues or serum and for affinity purification of PRO. The present
CC   sequence represents a PRO protein
XX
SQ   Sequence 437 AA;

  Query Match             100.0%;  Score 2381;  DB 5;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 9
ABG91359
ID   ABG91359 standard; protein; 437 AA.
XX
AC   ABG91359;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Novel human secreted protein #5.
XX
KW   Human; secreted protein; transmembrane protein; gene mapping; transgenic;
KW   immunogenic.
XX
OS   Homo sapiens.
XX
PN   US2002098505-A1.
XX
PD   25-JUL-2002.
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XX
PF   28-DEC-2001; 2001US-00033246.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI   Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-665999/71.
DR   N-PSDB; ABS67458.
XX
PT   New human secreted and transmembrane (PRO) polypeptides, useful for
PT   treating conditions requiring PRO polypeptides, for screening PRO
PT   antagonists and agonists useful as drug candidates.
XX
PS   Claim 12; Fig 10; 125pp; English.
XX
CC   The invention relates to new human secreted and transmembrane proteins
CC   (PRO) and nucleic acids of the invention. The polypeptides can be
CC   administered therapeutically, especially by expressing encoding
CC   polynucleotides, e.g. in therapeutic compositions. They can be used to
CC   screen for PRO polypeptide antagonists and agonists useful to identify
CC   drug candidates. They can also be used to produce antibodies, useful to
CC   detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
CC   therapeutically (e.g. as antagonists or to target and/or deliver
CC   cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
CC   produce antisense sequences to inhibit polypeptide production. They can
CC   be used to produce probes and primers useful to detect or isolate
CC   sequences encoding PRO polypeptides or similar sequences e.g. variants or
CC   sequences from other species. They are also useful for gene mapping and
CC   to generate transgenic animals. ABG91355-ABG91363 represent human PRO
CC   amino acid sequences of the invention
XX
SQ   Sequence 437 AA;

  Query Match            100.0%;  Score 2381;  DB 5;  Length 437;
  Best Local Similarity  100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 10
ABG31399
ID   ABG31399 standard; protein; 437 AA.
XX
AC   ABG31399;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human PRO1863 polypeptide.
XX
KW   Human; secreted and transmembrane polypeptide; PRO polypeptide;
KW   T-lymphocyte proliferation; inflammatory disease; rheumatoid arthritis;
KW   inflammatory bowel disease; Sjogren's syndrome; thyroiditis;
KW   autoimmune haemolytic anaemia; diabetes mellitus; multiple sclerosis;
KW   hepatitis; contact dermatitis; allergic disease; psoriasis; virucide;
KW   immune related disease; kidney disease; antiinflammatory; antithyroid;
KW   antirheumatic; antiarthritic; immunosuppressive; antianaemic;
KW   antidiabetic; neuroprotective; hepatotropic; antiinflammatory;
KW   dermatological; antiallergic; antipsoriatic; PRO1863.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .15
FT                   /label= Signal_peptide
FT   Protein         16. .437
FT                   /label= Mature_PRO1863
FT   Modified-site   46. .49
FT                   /note= "N-glycosylation site"
FT   Region          51. .54
FT                   /note= "Glycosaminoglycan attachment site"
FT   Modified-site   54. .59
FT                   /note= "N-myristoylation site"
FT   Modified-site   75. .80
FT                   /note= "N-myristoylation site"
FT   Modified-site   141. .146
FT                   /note= "N-myristoylation site"
FT   Modified-site   154. .159
FT                   /note= "N-myristoylation site"
FT   Modified-site   168. .173
FT                   /note= "N-myristoylation site"
FT   Modified-site   169. .174
FT                   /note= "N-myristoylation site"
FT   Modified-site   189. .192
FT                   /note= "N-glycosylation site"
FT   Modified-site   198. .203
FT                   /note= "N-myristoylation site"
FT   Domain          243. .260
```

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FT                   /label= Transmembrane_domain
FT   Modified-site   254. .259
FT                   /note= "N-myristoylation site"
FT   Modified-site   261. .266
FT                   /note= "N-myristoylation site"
FT   Modified-site   269. .274
FT                   /note= "N-myristoylation site"
FT   Modified-site   284. .289
FT                   /note= "N-myristoylation site"
FT   Modified-site   333. .338
FT                   /note= "N-myristoylation site"
FT   Modified-site   347. .352
FT                   /note= "N-myristoylation site"
FT   Region          359. .362
FT                   /note= "Glycosaminoglycan attachment site"
FT   Modified-site   360. .365
FT                   /note= "N-myristoylation site"
FT   Modified-site   361. .366
FT                   /note= "N-myristoylation site"
FT   Modified-site   382. .385
FT                   /note= "N-glycosylation site"
FT   Modified-site   388. .393
FT                   /note= "N-myristoylation site"
FT   Modified-site   408. .413
FT                   /note= "N-myristoylation site"
FT   Modified-site   419. .424
FT                   /note= "N-myristoylation site"
XX
PN   US2002098507-A1.
XX
PD   25-JUL-2002.
XX
PF   27-DEC-2001; 2001US-00033326.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-673823/72.
DR   N-PSDB; ABS53475.
XX
PT   Novel PRO polypeptides and nucleic acids encoding the polypeptides,
PT   useful for preparing a medicament for the treatment of inflammatory and
PT   immune related disorders.
XX
PS   Claim 12; Fig 10; 125pp; English.
XX
CC   The present invention relates to the isolation of novel human secreted
CC   and transmembrane polypeptides, designated PRO polypeptides, and the
CC   polynucleotide sequences encoding them. The PRO polypeptides of the
CC   invention include PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917,
CC   PRO1868, PRO3434 and PRO1927. The PRO polypeptides can inhibit the
CC   stimulation of T-lymphocyte proliferation. The PRO polypeptides are
CC   useful for the diagnosis and treatment of inflammatory diseases (e.g.
CC   inflammatory bowel disease, rheumatoid arthritis, Sjogren's syndrome,
CC   autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus, multiple
CC   sclerosis, hepatitis, contact dermatitis, allergic diseases and
CC   psoriasis), immune related diseases, and kidney diseases in humans. The
CC   present sequence represents human PRO1863 polypeptide
XX
SQ   Sequence 437 AA;

  Query Match             100.0%;  Score 2381;  DB 5;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 11
ADY31902
ID   ADY31902 standard; protein; 437 AA.
XX
AC   ADY31902;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1181.
XX
KW   PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer;
KW   lung; colon; breast; prostate; rectum; liver;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
KW   pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
KW   arthritis; sports injury; cytostatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO200193983-A1.
XX
```

PD 13-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017800.
XX
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 20-JUN-2000; 2000US-0212901P.
PR 22-JUN-2000; 2000US-0213807P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-404358/43.
DR N-PSDB; ADY31901.
XX
PT Isolated nucleic acid useful in a method for stimulating the
PT proliferation, gene expression or differentiation of cells and in
PT detecting the presence of a tumor.
XX
PS Claim 11; SEQ ID NO 162; 296pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. They are particularly useful for
CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
CC blood, for stimulating the proliferation or differentiation of
CC chondrocyte cells, for stimulating the proliferation of or gene
CC expression in pericyte cells or for stimulating the proliferation of
CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
CC technology, in generating transgenic animals or knock-out animals which
CC may be used in the development and screening of therapeutically useful
CC reagents, in gene therapy, in chromosome identification, as chromosome
CC markers and in generating probes. The PRO polypeptides, or anti-PRO
CC antibodies, are useful for preparing a medicament for treating a
CC condition which is responsive to the PRO polypeptides or anti-PRO
CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
CC differentiation of chondrocytes. The PRO polypeptides are useful as
CC molecular markers for protein electrophoresis, and in tissue typing. This
CC sequence represents a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent is also available in electronic format from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437
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RESULT 12
ABU72375
ID ABU72375 standard; protein; 437 AA.
XX
AC ABU72375;
XX
DT 16-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1863.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiinflammatory; dermatological; immunosuppressive; antirheumatic;
KW antiarthritic; haemostatic; antithyroid; neuroprotective; hepatotropic;
KW virucide; antipsoriatic; antiallergic; gene therapy; colon cancer;
KW inflammatory bowel disease; systemic lupus erythematosus; hepatitis;
KW rheumatoid arthritis; scleroderma; Sjogren's syndrome; thyroiditis;
KW thrombocytopaenia; multiple sclerosis; cystic fibrosis; psoriasis;
KW allergy; graft-versus-host disease; graft rejection.
XX
OS Homo sapiens.
XX
PN US2002182618-A1.
XX
PD 05-DEC-2002.
XX
PF 27-DEC-2001; 2001US-00033167.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.

```
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2003-328610/31.
DR   N-PSDB; ACA64082.
XX
PT   New secreted and transmembrane PRO polypeptides or genes encoding them,
PT   useful for treating e.g. colon cancer, inflammatory bowel disease,
PT   Sjogren's syndrome, thrombocytopenia, thyroiditis, multiple sclerosis or
PT   graft rejection.
XX
PS   Claim 12; Fig 10; 119pp; English.
XX
CC   The invention describes an isolated secreted and transmembrane
CC   polypeptide (PRO), which scores at least 80% amino acid sequence identity
CC   when compared to: (a) a sequence comprising 278, 830, 125, 325, 437, 487,
CC   310, 1029 or 548 amino acids fully defined in the specification; (b) any
CC   of the sequences of (a), lacking its associated signal peptide; (c) an
CC   extracellular domain of (a), with or lacking its associated signal
CC   peptide. The PRO polypeptide or polynucleotide is useful as
CC   pharmaceuticals or diagnostics. These are particularly useful for
CC   treating colon cancer, inflammatory bowel disease, systemic lupus
CC   erythematosus, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC   thrombocytopaenia, thyroiditis, multiple sclerosis, hepatitis, cystic
CC   fibrosis, psoriasis, allergies, graft-versus-host disease or graft
CC   rejection in a mammal. This is the amino acid sequence of a novel human
CC   secreted and transmembrane PRO polypeptide
XX
SQ   Sequence 437 AA;

  Query Match            100.0%;  Score 2381;  DB 6;  Length 437;
  Best Local Similarity  100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
              |||||||||||||||||
Db        421 GLALAPALWWGVVCPSC 437


RESULT 13
ABU58075
ID   ABU58075 standard; protein; 437 AA.
XX
AC   ABU58075;
XX
DT   14-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #107.
XX
KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW   horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027163-A1.
XX
PD   06-FEB-2003.
XX
PF   15-NOV-2001; 2001US-00997666.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
PR   02-JUN-1998;   98US-0087607P.
PR   02-JUN-1998;   98US-0087609P.
PR   02-JUN-1998;   98US-0087759P.
PR   03-JUN-1998;   98US-0087827P.
PR   04-JUN-1998;   98US-0088021P.
PR   04-JUN-1998;   98US-0088025P.
PR   04-JUN-1998;   98US-0088026P.
PR   04-JUN-1998;   98US-0088028P.
PR   04-JUN-1998;   98US-0088029P.
PR   04-JUN-1998;   98US-0088030P.
PR   04-JUN-1998;   98US-0088033P.
PR   04-JUN-1998;   98US-0088326P.
PR   05-JUN-1998;   98US-0088167P.
PR   05-JUN-1998;   98US-0088202P.
PR   05-JUN-1998;   98US-0088212P.
PR   05-JUN-1998;   98US-0088217P.
PR   09-JUN-1998;   98US-0088655P.
PR   10-JUN-1998;   98US-0088734P.
PR   10-JUN-1998;   98US-0088738P.
PR   10-JUN-1998;   98US-0088742P.
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PR 11-JUN-1998; 98US-0088858P.
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PR 07-OCT-1998; 98WO-US021141.
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PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
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PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
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PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

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Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
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Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
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Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
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Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
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Db        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420

Qy        421 GLALAPALWWGVVCPSC 437
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Db        421 GLALAPALWWGVVCPSC 437


RESULT 14
ABU59153
ID   ABU59153 standard; protein; 437 AA.
XX
AC   ABU59153;
XX
DT   28-APR-2003  (first entry)
XX
DE   Novel human secreted or transmembrane protein PRO1181.
XX
KW   Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW   cardiac insufficiency disorder; cancer; tumour; immune response;
KW   adrenal cortical capillary endothelial growth; c-fos induction;
KW   vascular endothelial growth factor inhibition; VEGF inhibition;
KW   endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW   retinal neurons cell survival; rod photoreceptor cell survival;
KW   retinal disorder; retinitis pigmentosum; kidney disorder;
KW   mammalian kidney mesangial cell proliferation; Berger disease;
KW   dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW   chondrocyte redifferentiation; sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002132252-A1.
XX
PD   19-SEP-2002.
XX
PF   14-NOV-2001; 2001US-00990442.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
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PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
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PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
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PR   01-DEC-1999;   99WO-US028634.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   06-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
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PR   02-MAR-2000; 2000WO-US005841.
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PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
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PR   30-MAY-2000; 2000WO-US014941.
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PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
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PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   28-AUG-2001; 2001US-00941992.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2003-247083/24.
DR   N-PSDB; ABX80352.
XX
PT   Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT   and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT   are therapeutically useful for enhancing immune response and in cancer
PT   treatments.
XX
PS   Claim 12; Fig 250; 648pp; English.
XX
CC   The invention describes an isolated human PRO polypeptide. The PRO
CC   polypeptides are useful in detecting PRO polypeptides in a sample, in
CC   linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC   in modulating at least one biological activity of a cell expressing a PRO
CC   polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC   useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC   stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC   PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC   PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC   useful for treating conditions or disorders where angiogenesis would be
CC   beneficial, e.g. wound healing and antagonist of this polypeptide are
CC   useful for treating cancerous tumours. PRO812 inhibits vascular
CC   endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC   cells and is thus useful for inhibiting endothelial cell growth in
CC   mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC   PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC   stimulated T-lymphocytes and are therapeutically useful for enhancing
CC   immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC   retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC   rod photoreceptor cells) and therefore are useful for treating retinal
CC   disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC   and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC   and therefore are useful for treating kidney disorders associated with
CC   decreased mesangial cell function such as Berger disease or other
CC   nephropathies associated with dermatitis, herpetiformis or Crohn's
CC   disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC   proliferation and/or redifferentiation of chondrocytes in culture and are
CC   thus useful for treating sports injuries, and arthritis. This is the
CC   amino acid sequence of a novel human PRO protein
XX
SQ   Sequence 437 AA;

  Query Match             100.0%;  Score 2381;  DB 6;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-172;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
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Db          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60

Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
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Db        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240

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Db        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300

Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
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Db        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360

Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
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Qy        421 GLALAPALWWGVVCPSC 437
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Db        421 GLALAPALWWGVVCPSC 437


RESULT 15
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ID   ABU80865 standard; protein; 437 AA.
XX
AC   ABU80865;
XX
DT   23-JUN-2003  (first entry)
XX
DE   Human secreted and transmembrane polypeptide PRO1863.
XX
KW   Human; gene therapy; inflammatory disease; Crohn's disease;
KW   inflammatory bowel disease; ulcerative colitis; tumour; cancer;
KW   colorectal cancer.
XX
OS   Homo sapiens.
XX
PN   US2002192668-A1.
XX
PD   19-DEC-2002.
XX
PF   27-DEC-2001; 2001US-00033244.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
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PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
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PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
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PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2003-328857/31.
DR N-PSDB; ACA66975.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammatory diseases, tumors or cancer.
XX
PS Claim 12; Fig 10; 119pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases such as inflammatory bowel disease, ulcerative
CC colitis and Crohn's disease, tumours, or cancer such as colorectal
CC cancer. The nucleic acids are useful as hybridisation probes, in
CC chromosome and gene mapping and in generating antisense RNA or DNA. The
CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. Both are useful in tissue typing. The present sequence
CC represents the amino acid sequence of a PRO polypeptide of the invention
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 6; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        421 GLALAPALWWGVVCPSC 437
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Search completed: July 11, 2006, 09:24:50
Job time : 199 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:30:57 ; Search time 185 Seconds
(without alignments)
1094.189 Million cell updates/sec

Title: US-10-727-619-2
Perfect score: 2381
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2381	100.0	437	3	US-09-989-279-355	Sequence 355, App
4	2381	100.0	437	3	US-09-989-727-355	Sequence 355, App
5	2381	100.0	437	3	US-09-989-731-355	Sequence 355, App
6	2381	100.0	437	3	US-09-989-732-355	Sequence 355, App
7	2381	100.0	437	3	US-09-991-073-355	Sequence 355, App
8	2381	100.0	437	3	US-09-990-442-355	Sequence 355, App
9	2381	100.0	437	3	US-09-991-163-355	Sequence 355, App
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23	2381	100.0	437	3	US-09-989-724-355	Sequence 355, App
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ALIGNMENTS

RESULT 1
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; Sequence 355, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;  PRIOR FILING DATE: 1998-07-09

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RESULT 2
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; Patent No. US20020072092A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C62
;  CURRENT APPLICATION NUMBER: US/09/989,723
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 2381; DB 3; Length 437;
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David

; APPLICANT: Desnoyers,Luc
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; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Gerritsen,Mary E.
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; APPLICANT: Paoni,Nicholas F.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
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;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
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;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
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;  TITLE OF INVENTION:  Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
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; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1998-07-09

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RESULT 6
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; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.

; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
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;  TITLE OF INVENTION:  Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 355, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
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; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
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Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

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RESULT 10
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; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
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Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
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RESULT 11
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; Sequence 355, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C22
;  CURRENT APPLICATION NUMBER: US/09/990,456
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
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Db         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
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Db        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV 240
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Qy        241 GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN 300
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Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
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RESULT 12
US-09-989-721-355
; Sequence 355, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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RESULT 13
US-09-992-598-355
; Sequence 355, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020177164A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C66
;  CURRENT APPLICATION NUMBER: US/09/989,293A
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

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Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
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Qy        421 GLALAPALWWGVVCPSC 437
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RESULT 15
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; Sequence 355, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM 60
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Qy         61 LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
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Qy        121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 GLALAPALWWGVVCPSC 437
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Search completed: July 11, 2006, 09:34:47
Job time : 187 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 10:29:39 ; Search time 1048 Seconds
(without alignments)
10644.654 Million cell updates/sec

Title: US-10-727-619-1
Perfect score: 1600
Sequence: 1 aaaagcagaaagagattacc.....ctgataatacagaccctgtc 1600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
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8: geneseqn2003as:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1600	100.0	1600	3	AAA12386	Aaa12386 Human PRV
2	1600	100.0	1600	4	AAF61560	Aaf61560 Human PRV
3	1599.6	100.0	1630	12	ADQ21061	Adq21061 Human sof
4	1599.6	100.0	1630	14	AEA04409	Aea04409 Human cDN
5	1598.4	99.9	1692	12	ADQ24979	Adq24979 Human sof
6	1584	99.0	1612	6	ABA97156	Aba97156 Human gra
7	1579.4	98.7	1587	3	AAZ65083	Aaz65083 Membrane-
8	1579.4	98.7	1587	3	AAA51263	Aaa51263 Human DNA
9	1579.4	98.7	1587	4	AAS21476	Aas21476 Human cDN
10	1579.4	98.7	1587	5	AAF44229	Aaf44229 Human PRO
11	1579.4	98.7	1587	6	ABK33616	Abk33616 cDNA enco
12	1579.4	98.7	1587	6	ABS68390	Abs68390 Human cDN
13	1579.4	98.7	1587	6	ABS67458	Abs67458 cDNA enco
14	1579.4	98.7	1587	6	ABS53475	Abs53475 cDNA enco
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16	1579.4	98.7	1587	8	ACA64398	Aca64398 Novel hum
17	1579.4	98.7	1587	8	ACA03835	Aca03835 cDNA enco
18	1579.4	98.7	1587	8	ABX11171	Abx11171 cDNA enco
19	1579.4	98.7	1587	8	ABX89373	Abx89373 DNA encod
20	1579.4	98.7	1587	8	ABX80857	Abx80857 Human sec
21	1579.4	98.7	1587	8	ACD44366	Acd44366 cDNA enco
22	1579.4	98.7	1587	8	ACD42027	Acd42027 Human sec
23	1579.4	98.7	1587	8	ACA68577	Aca68577 Novel hum
24	1579.4	98.7	1587	8	ABX79537	Abx79537 Human sec
25	1579.4	98.7	1587	8	ABX90607	Abx90607 Human sec
26	1579.4	98.7	1587	8	ACA93558	Aca93558 Novel hum
27	1579.4	98.7	1587	8	ABX81240	Abx81240 Novel hum
28	1579.4	98.7	1587	8	ACA04256	Aca04256 Human cDN
29	1579.4	98.7	1587	8	ACA67365	Aca67365 cDNA enco
30	1579.4	98.7	1587	8	ACA93056	Aca93056 Novel hum
31	1579.4	98.7	1587	8	ABX17140	Abx17140 Human PRO
32	1579.4	98.7	1587	9	ACA67995	Aca67995 Novel hum
33	1579.4	98.7	1587	9	ACA88444	Aca88444 Human sec
34	1579.4	98.7	1587	9	ACD81951	Acd81951 cDNA enco
35	1579.4	98.7	1587	9	ADA45984	Ada45984 Novel hum
36	1579.4	98.7	1587	9	ADA76415	Ada76415 Human PRO
37	1579.4	98.7	1587	9	ABT44306	Abt44306 Human PRO
38	1579.4	98.7	1587	9	ADA19065	Ada19065 Human PRO
39	1579.4	98.7	1587	9	ADA61688	Ada61688 Homo sapi
40	1579.4	98.7	1587	9	ADB19473	Adb19473 Novel hum
41	1579.4	98.7	1587	9	ADB28014	Adb28014 cDNA enco
42	1579.4	98.7	1587	9	ADA86493	Ada86493 Novel hum
43	1579.4	98.7	1587	9	ADB16057	Adb16057 Human PRO
44	1579.4	98.7	1587	9	ADA37865	Ada37865 Human cDN
45	1579.4	98.7	1587	9	ADA47843	Ada47843 Human PRO

ALIGNMENTS

RESULT 1
AAA12386
ID AAA12386 standard; DNA; 1600 BP.
XX
AC AAA12386;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human PRV-1 DNA.
XX
KW PRV-1; human; polycythaemia rubra vera; PRV; antiproliferative;
KW treatment; detection; diagnosis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 36. .1349
FT /*tag= a
FT /product= "PRV-1"
XX
PN DE19849044-A1.
XX
PD 27-APR-2000.
XX
PF 23-OCT-1998; 98DE-01049044.
XX
PR 23-OCT-1998; 98DE-01049044.
XX
PA (UYFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
XX
PI Pahl H, Temerinac S;
XX
DR WPI; 2000-319347/28.
DR P-PSDB; AAY87750.
XX
PT New polycythemia rubra vera-related polypeptide useful for diagnosis and
PT for developing therapeutic antibodies.
XX
PS Claim 1; Fig 1; 6pp; German.
XX
CC This invention describes a novel PRV-1 protein (I) detected in humans

```
CC   suffering from the condition polycythaemia rubra vera (PRV). The product
CC   of the invention has antiproliferative activity. The encoding nucleic
CC   acid sequence is used to express recombinant PRV-1 polypeptides and as a
CC   source of antisense sequences that can be expressed in vivo for treatment
CC   of PRV. (I) is used to raise specific mono or polyclonal antibodies and
CC   these are used to diagnose PRV (by detecting (I), or its epitopes, in
CC   immunoassays) or for treatment of PRV (optionally when coupled to a
CC   cytotoxin). This sequence encodes the human PRV-1 protein described in
CC   the method of the invention
XX
SQ   Sequence 1600 BP; 340 A; 490 C; 437 G; 333 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1600;  DB 3;  Length 1600;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1600;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
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Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
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Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
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Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
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Db        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
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Db        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
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Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
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Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
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Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
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Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
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Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
              ||||||||||||||||||||||||||||||||||||||||
Db       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600


RESULT 2
AAF61560
ID   AAF61560 standard; DNA; 1600 BP.
XX
AC   AAF61560;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Human PRV-1 encoding DNA.
XX
KW   PRV-1; human; hemostatic; polycythemia rubra vera; antisense therapy;
KW   treatment; diagnosis; pancytopenia; bone-marrow; blood; growth factor;
KW   pancytopathy; hematopoietic system disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             36. .1349
FT                   /*tag=  a
FT                   /product= "PRV-1"
XX
```

PN DE19947010-A1.
XX
PD 05-APR-2001.
XX
PF 30-SEP-1999; 99DE-01047010.
XX
PR 30-SEP-1999; 99DE-01047010.
XX
PA (UYFR-) UNIV FREIBURG.
XX
PI Pahl H;
XX
DR WPI; 2001-246167/26.
DR P-PSDB; AAB70851.
XX
PT New cloned PRV-1 gene associated with polycythemia rubra vera, e.g.
PT useful for preparing antisense molecules or polypeptides for treatment or
PT diagnosis of disorders of the hematopoietic system.
XX
PS Claim 4; Fig 1; 10pp; German.
XX
CC This invention describes a novel cloned PRV-1 gene (I) which has
CC hemostatic activity and is associated with polycythemia rubra vera (PRV).
CC (I) is useful for: (1) producing a recombinant PRV-1 polypeptide; (2)
CC producing antisense molecules useful for diagnosis and treatment of PRV;
CC (3) preparing medicaments for treating pancytopenias and pancytopathies
CC of the bone-marrow and blood. The polypeptide is useful: (1) as a growth
CC factor for inducing hematopoietic stem cells to form erythroid colonies;
CC (2) for preparing medicaments for treating pancytopenias and
CC pancytopathies of the bone-marrow and blood; (3) for treating and/or
CC multiplying autologous cells and/or established cell lines ex vivo or in
CC vitro; and (4) for producing antibodies useful for diagnosis of PRV or
CC other disorders of the hematopoietic system. This sequence encodes the
CC human PRV-1 protein described in the invention
XX
SQ Sequence 1600 BP; 340 A; 490 C; 437 G; 333 T; 0 U; 0 Other;

Query Match 100.0%; Score 1600; DB 4; Length 1600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240

Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300

Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420

Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGGTGCTTGTGGCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGGTGCTTGTGGCCT 900

Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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Db       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600

RESULT 3
ADQ21061
ID   ADQ21061 standard; DNA; 1630 BP.
XX
AC   ADQ21061;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 3881.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2004048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 3881; 210pp; English.
XX
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in both soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   DNA of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
SQ   Sequence 1630 BP; 365 A; 492 C; 436 G; 336 T; 0 U; 1 Other;

  Query Match           100.0%;  Score 1600;  DB 12;  Length 1630;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1599;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240

Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300

Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420

Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Qy        661 TGACCTGTCATCGGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGACCTGTCATCGGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGGTGCTTGTGGCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGGTGCTTGTGGCCT 900

Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
             ||||||:|||||||||||||||||||||||||||||||||
Db       1561 GGAGGARTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
```

RESULT 4
AEA04409
ID AEA04409 standard; cDNA; 1630 BP.
XX
AC AEA04409;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human cDNA from gene under-expressed in cancer, PRV1.
XX
KW Tumor marker; ss; gene; colon tumor; cancer; cytostatic; neoplasm;
KW diagnostic; microarray; drug screening.
XX
OS Homo sapiens.
XX
PN WO2005044990-A2.
XX
PD 19-MAY-2005.
XX
PF 01-NOV-2004; 2004WO-US036404.
XX
PR 04-NOV-2003; 2003US-00700439.
XX
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Burgess C, Myerow S, Thiagalingam A, Maimonis P, Molino G;
PI Burgart L, Boardman LA, Thibodeau S, Lewis M;
XX
DR WPI; 2005-372198/38.
DR P-PSDB; AEA04502.
DR REFSEQ; NM_020406.
XX
PT Detecting expression of one or more nucleic acid sequences in biological
PT sample, useful for detecting cancer, comprises detecting a change in the
PT expression level of one or more nucleic acid sequences relative to a
PT control expression level.
XX
PS Claim 1; SEQ ID NO 54; 256pp; English.
XX
CC The invention relates to detecting differential expression of one or more
CC nucleic acid sequences (appearing as AEA04356-AEA04448 in a biological
CC sample comprising obtaining the sample from a subject, and detecting a
CC change in the expression level of one or more nucleic acid sequences
CC relative to a control expression level of the nucleic acid sequences, is
CC new. Also included are detecting cancer (or a pre-malignant condition
CC thereof) in a subject (comprising comparing the expression level of one
CC or more nucleic acid sequences in a biological sample from the subject
CC with a control expression level of the nucleic acid sequences, where a
CC change of at least two-fold in the expression level of the nucleic acid
CC sequences is indicative of cancer or pre-malignant condition), monitoring
CC the onset (or progression, or regression) of cancer (or a pre-malignant
CC condition) in a subject (by detecting in a biological sample of the
CC subject at a first point in time the expression of one or more nucleic
CC acid sequences, repeating the first step at a subsequent point in time
CC and comparing the expression level detected, where a change in the
CC expression level is indicative of progression of cancer or its pre-
CC malignant condition in the subject), determining prognosis for cancer or
CC its pre-malignant condition in a subject (comprising detecting in a
CC biological sample of the subject, the expression level of one or more
CC nucleic acid sequences, comparing the expression level with a reference
CC expression level of the nucleic acid sequences and evaluating the
CC prognosis of the subject based on the comparison), determining the
CC efficacy of a test compound for inhibiting cancer in a subject,
CC determining the efficacy of a therapy for inhibiting cancer in a subject,
CC selecting a composition for inhibiting cancer in a subject, inhibiting
CC cancer in a subject, a polypeptide encoded by the nucleic acids above
CC (appearing as AEA04449-AEA04541), an antibody that specifically binds to
CC the polypeptide sequence, and detecting in a biological sample the
CC presence of a polypeptide. The method is useful for detecting
CC differential expression of one or more nucleic acid sequences in a
CC biological sample, which is useful for detecting cancer (especially colon
CC cancer), monitoring the onset, progression, or regression of cancer or a
CC pre-malignant condition, or determining prognosis for cancer or its pre-
CC malignant condition in a subject, or for determining the efficacy of a
CC test compound for inhibiting cancer in a subject. The compound is useful
CC for inhibiting cancer in a subject. The antibodies may also be used to
CC treat cancer. The present sequence is a cDNA from a human gene under-
CC expressed in cancer samples.
XX
SQ Sequence 1630 BP; 365 A; 492 C; 436 G; 336 T; 0 U; 1 Other;

Query Match 100.0%; Score 1600; DB 14; Length 1630;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1599; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240

Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300

Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420

Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
```

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Db        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Db        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Db        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900

Db        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900

Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Db        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600

Db       1561 GGAGGARTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600

RESULT 5
ADQ24979
ID   ADQ24979 standard; DNA; 1692 BP.
XX
AC   ADQ24979;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7799.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2004048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 7799; 210pp; English.
XX
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in both soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   DNA of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
SQ   Sequence 1692 BP; 427 A; 493 C; 436 G; 336 T; 0 U; 0 Other;

  Query Match           99.9%;  Score 1598.4;  DB 12;  Length 1692;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCC 60

Db          1 AAAAGCAGAAAGAGATTACCAGCCACAGACGGGTCATGAGCCCGGTATTACTGCTGGCCC 60

Qy         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Db         61 TCCTGGGGTTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120

Qy        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Db        121 TTCAGCATGTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCT 180

Qy        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240

Db        181 GCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGA 240

Qy        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300
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Db        241 GCCTGGTGCTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGC 300

Qy        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACT 360

Qy        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAG 420

Qy        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCCTTGAGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAG 480

Qy        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAG 540

Qy        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCA 600

Qy        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660

Qy        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTG 720

Qy        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGC 780

Qy        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTG 840

Qy        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCT 900

Qy        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGC 960

Qy        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTG 1020

Qy       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080

Qy       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCA 1140

Qy       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGA 1200

Qy       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTG 1260

Qy       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGT 1320

Qy       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGC 1380

Qy       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGACCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATT 1440

Qy       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTTTCCCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCT 1500

Qy       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AACAGCAACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCT 1560

Qy       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
              ||||||||||||||||||||||||||||||||||||||||
Db       1561 GGAGGAGTGGCTGCATGTATCTGATAATACAGACCCTGTC 1600
```

RESULT 6
ABA97156
ID ABA97156 standard; cDNA to mRNA; 1612 BP.
XX
AC ABA97156;
XX
DT 17-APR-2002 (first entry)
XX
DE Human granulocyte HNA-2a antigen cDNA.
XX
KW Human; gene; neutrophilic granulocyte; chromosome 19; HNA-2a; antigen;
KW human neutrophil antigen-2a; NB-1 antigenic determination; diagnosis;
KW alloantibody detection; neonatal; immunoneutropaenia; iatrogenic;
KW transplant-associated acute pulmonary insufficiency;
KW bone marrow transplant; autoimmunoneutropaenia; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   28. .1341
FT   /*tag= c
FT   /product= "HNA-2a antigen (previously called NB-1)"
FT sig_peptide   28. .90
FT   /*tag= a
FT mat_peptide   91. .1338
FT   /*tag= b
XX
PN DE10028725-A1.
XX
PD 13-DEC-2001.
XX
PF 09-JUN-2000; 2000DE-01028725.
XX
PR 09-JUN-2000; 2000DE-01028725.
XX
PA (BUXJ/) BUX J.
XX
PI Bux J, Kissel K;
XX
DR WPI; 2002-148930/20.
DR P-PSDB; AAG80767.
XX
PT Primary structure and nucleic acid of the human neutrophil antigen-2a,
PT useful for antigen detection, e.g. diagnosis of various forms of
PT neutropenia.
XX
PS Disclosure; Page 4-6; 8pp; German.
XX
CC This invention describes the human neutrophil antigen-2a (HNA-2a,
CC previously described as NB-1), expressed on neutrophilic granulocytes.
CC The nucleic acid and amino acid sequences of NHA-2a are used in RNA- or
CC DNA-based methods of antigen determination, e.g. polymerase chain
CC reaction with sequence-specific primers, hybridisation with sequence-
CC specific oligonucleotides or DNA sequencing. They are also used for
CC recombinant production of the antigen for detection of specific

```
CC   alloantibodies. Allo- and auto-antibodies against HNA-2a are implicated
CC   in neonatal immunoneutropaenia, transplant-associated acute pulmonary
CC   insufficiency, immunoneutropaenia after bone marrow transplant,
CC   iatrogenic immunoneutropaenia and autoimmunoneutropaenia. Using NHA-2a,
CC   or its nucleic acid, for diagnosis, overcomes the stability problems
CC   associated with use and transport of very unstable granulocytes. The
CC   nucleic acid also allows large-scale production of the antigen. This
CC   sequence encodes the human granulocyte HNA-2a (NB-1) antigen found on
CC   chromosome 19 described in the invention
XX
SQ   Sequence 1612 BP; 351 A; 491 C; 433 G; 337 T; 0 U; 0 Other;

  Query Match             99.0%;  Score 1584;  DB 6;  Length 1612;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1587;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 AAAGAGATTACCAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGG 68
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 AAAGAGATTACCAGCCACAGACGGGTCATGAGCCCGGTATTACTGCTGGCCCTCCTGGGG 60

Qy         69 TTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCAT 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCATCCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCAT 120

Qy        129 GTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGC 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGTGGAAGGTGTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGC 180

Qy        189 GGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTG 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTG 240

Qy        249 CTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATG 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTCCAAGGGCTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATG 300

Qy        309 GGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAAC 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCCCCGGCCTCTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAAC 360

Qy        369 AACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTG 428
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        361 AACCTCGTTAACTCCCTCCCGTTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTG 420

Qy        429 AGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGC 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTGCCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGC 480

Qy        489 CCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTC 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTC 540

Qy        549 TCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACA 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACA 600

Qy        609 CAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGT 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGT 660

Qy        669 CATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACC 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACC 720

Qy        729 ACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATA 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATA 780

Qy        789 GATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAA 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAA 840

Qy        849 AATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACC 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACC 900

Qy        909 CACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCC 968
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Db        901 CACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCC 960

Qy        969 CTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCC 1028
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Db        961 CTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCAGCAGTGTCCTACCTGTGTGCAGCCC 1020

Qy       1029 CTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGT 1088
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Db       1021 CTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGT 1080

Qy       1089 TATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGC 1148
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Db       1081 TATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGC 1140

Qy       1149 TGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCT 1208
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Db       1141 TGCGTGGCCCAACCTTCCAGCTCCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCT 1200

Qy       1209 GCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAG 1268
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Qy       1269 GGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGA 1328
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Qy       1329 GTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACC 1388
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Qy       1389 CACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCA 1448
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Qy       1449 TTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAA 1508
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Db       1441 TTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTATTCACCTAACAGCAA 1500

Qy       1509 CACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGT 1568
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Db       1501 CACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGT 1560

Qy       1569 GGCTGCATGTATCTGATAATACAGACCCTGTC 1600
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Db       1561 GGCTGCATGTATCTGATAATACAGACCCTGTC 1592


RESULT 7
AAZ65083
ID   AAZ65083 standard; cDNA; 1587 BP.
XX
AC   AAZ65083;
XX
DT   05-APR-2000  (first entry)
XX
DE   Membrane-bound protein PRO1181 encoding cDNA.
XX
KW   Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW   pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO9963088-A2.
XX
PD   09-DEC-1999.
XX
PF   02-JUN-1999;   99WO-US012252.
XX
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PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR P-PSDB; AAY66737.
XX
PT Membrane-bound proteins and related nucleotide sequences.

```
XX
PS   Claim 2; Fig 249; 822pp; English.
XX
CC   The invention provides membrane-bound PRO polypeptides and
CC   polynucleotides encoding them. The PRO sequences of the invention were
CC   identified based on extracellular domain homology screening. The PRO
CC   sequences have homology with proteins including LDL receptors, TIE
CC   ligands and various enzymes. The membrane-bound proteins and receptor
CC   molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC   immunoadhesins, for instance, can be used as therapeutic agents to block
CC   receptor-ligand interactions. The membrane-bound proteins can also be
CC   employed for screening of potential peptide or small molecule inhibitors
CC   of the relevant receptor/ligand interaction. The PRO encoding sequences
CC   are useful as hybridization probes, in chromosome and gene mapping and in
CC   the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC   also be useful for the preparation of PRO polypeptides, especially by
CC   recombinant techniques
XX
SQ   Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

  Query Match             98.7%;  Score 1579.4;  DB 3;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
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Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
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Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
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Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
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Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
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Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
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Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
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Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
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Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
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Db       1561 TCTGATAATACAGACCCTGTC 1581


RESULT 8
AAA51263
ID   AAA51263 standard; cDNA; 1587 BP.
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AC   AAA51263;
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DT   26-SEP-2000  (first entry)
XX
DE   Human DNA encoding PRO1863, a novel transmembrane protein.
XX
KW   PRO1863; secreted protein; transmembrane protein; recombinant production;
KW   gene therapy; ss.
XX
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OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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FT                   /product= "PRO1863"
FT                   /note= "A novel transmembrane protein"
FT   sig_peptide     17. .61
FT                   /*tag=  b
XX
PN   WO200036102-A2.
XX
PD   22-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US028634.
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PR   16-DEC-1998;   98US-0112851P.
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PR   12-JAN-1999;   99US-0115558P.
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PR   09-FEB-1999;   99US-0119341P.
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PR   02-JUN-1999;   99WO-US012252.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2000-431586/37.
DR   P-PSDB; AAY96733.
XX
PT   Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT   transmembrane polypeptide.
XX
PS   Claim 1; Fig 9; 154pp; English.
XX
CC   This cDNA encodes PRO1863, a novel transmembrane protein. The invention
CC   concerns novel secreted and transmembrane proteins, designated PRO
CC   polypeptides. The cDNA and gene sequences are useful in the recombinant
CC   production of PRO polypeptides, as a hybridization probe to screen
CC   libraries to isolate cDNAs with sequence identity to PRO polypeptides or
CC   to map the gene encoding the PRO polypeptides and analyzing genetic
CC   disorders. The cDNA/gene can also be used to produce transgenic animals
CC   useful for the development and screening of therapeutically useful
CC   reagents. They can also be used in gene therapy, e.g. to replace a
CC   defective gene
XX
SQ   Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

  Query Match             98.7%;  Score 1579.4;  DB 3;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
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Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320
```

```
Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
             ||||||||||||||||||||
Db       1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 9
AAS21476
ID AAS21476 standard; cDNA; 1587 BP.
XX
AC AAS21476;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO1181 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR P-PSDB; AAU12404.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 3; Fig 465; 813pp; English.
XX
CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 4; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGGTTCATCCTCCC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300
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Qy       320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy       380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy       440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy       500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy       560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy       620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy       680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy       740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy       800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy       860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy       920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy       980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy      1040 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TTCAAGTGGCTCCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy      1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy      1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy      1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy      1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy      1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy      1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy      1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy      1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy      1580 TCTGATAATACAGACCCTGTC 1600
            ||||||||||||||||||||
Db      1561 TCTGATAATACAGACCCTGTC 1581
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RESULT 10
AAF44229
ID AAF44229 standard; cDNA; 1587 BP.
XX
AC AAF44229;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1181 (UNQ595) nucleotide sequence SEQ ID NO:354.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.

```
DR   P-PSDB; AAB65260.
XX
PT   PRO polynucleotides used to produce polypeptides used to target bioactive
PT   molecules such as toxins, radiolabels or antibodies, to specific cells,
PT   to cause targeted cell death.
XX
PS   Claim 2; Fig 249; 935pp; English.
XX
CC   The present invention describes human secreted and transmembrane PRO
CC   proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC   be used for targeted delivery of bioactive molecules, such as toxins,
CC   radiolabels or antibodies, that cause cell death. PRO nucleotide
CC   sequences, and their fragments, can be used as hybridisation probes, in
CC   chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC   DNA. They may also be used to produce transgenic animals which are used
CC   to develop and screen therapeutically useful reagents. The PRO nucleotide
CC   and protein sequence can be used for tissue typing and in treating
CC   cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC   AAF44470 represent PCR primers and hybridisation probes used in the
CC   isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC   AAB65300 represent human PRO polynucleotide and protein sequences given
CC   in the exemplification of the present invention
XX
SQ   Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

  Query Match             98.7%;  Score 1579.4;  DB 5;  Length 1587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1580;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
              |||||||||||||||||||||
Db       1561 TCTGATAATACAGACCCTGTC 1581


RESULT 11
ABK33616
ID   ABK33616 standard; cDNA; 1587 BP.
XX
AC   ABK33616;
XX
DT   08-MAY-2002  (first entry)
XX
```

DE cDNA encoding human PRO protein, Seq ID No 161.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR P-PSDB; AAU83672.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
PS Claim 2; Fig 161; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO
CC protein coding sequences of the invention
XX

SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 6; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGGTTCATCCTCCC 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
               ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020
```

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Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
             ||||||||||||||||||||
Db       1561 TCTGATAATACAGACCCTGTC 1581
```

RESULT 12
ABS68390
ID ABS68390 standard; cDNA; 1587 BP.
XX
AC ABS68390;
XX
DT 18-NOV-2002 (first entry)
XX
DE Human cDNA encoding secreted protein PRO1863.
XX
KW Human; ss; gene; secreted and transmembrane protein; PRO1800; PRO539;
KW PRO982; PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW inflammatory disorder; immune related disease; rheumatoid arthritis;
KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW psoriasis; allergic disease of the lung; graft-versus host disease;
KW tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002098506-A1.
XX
PD 25-JUL-2002.
XX
PF 27-DEC-2001; 2001US-00033301.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2002-690475/74.
DR P-PSDB; ABG92707.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides useful
PT for diagnosis and treatment of inflammatory disorders and immune-related
PT diseases, and identifying modulators.
XX
PS Claim 2; Fig 9; 125pp; English.
XX
CC The invention relates to an isolated polypeptide having at least 80%
CC amino acid sequence identity to secreted and transmembrane polypeptides
CC PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
CC cells and antibodies against PRO polypeptides. PRO proteins are useful
CC for identifying modulators of the polypeptide. PRO1868 useful for the
CC diagnosis and treatment of inflammatory and immune related diseases
CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
CC sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
CC infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
CC versus host disease and tumours. Pro nucleic acids are useful for
CC constructing hybridisation probes for mapping the gene that encodes that
CC PRO and for the genetic analysis of individuals with genetic disorders,
CC and for generating transgenic animals which are useful in the development
CC and screening of therapeutically useful reagents. PRO nucleic acids are
CC also useful for gene therapy, chromosome identification, and tissue
CC typing. PRO proteins are useful as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies are useful in
CC diagnostic assays for PRO, e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO. The present
CC sequence encodes a PRO protein
XX
SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 6; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
              ||||||||||||||||||||
Db       1561 TCTGATAATACAGACCCTGTC 1581
```

RESULT 13
ABS67458
ID ABS67458 standard; cDNA; 1587 BP.
XX
AC ABS67458;
XX
DT 29-NOV-2002 (first entry)
XX
DE cDNA encoding novel human secreted protein #5.
XX
KW Human; secreted protein; transmembrane protein; gene mapping; transgenic;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2002098505-A1.
XX
PD 25-JUL-2002.
XX
PF 28-DEC-2001; 2001US-00033246.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH) GENENTECH INC.

XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2002-665999/71.
DR P-PSDB; ABG91359.
XX
PT New human secreted and transmembrane (PRO) polypeptides, useful for
PT treating conditions requiring PRO polypeptides, for screening PRO
PT antagonists and agonists useful as drug candidates.
XX
PS Claim 2; Fig 9; 125pp; English.
XX
CC The invention relates to new human secreted and transmembrane proteins
CC (PRO) and nucleic acids of the invention. The polypeptides can be
CC administered therapeutically, especially by expressing encoding
CC polynucleotides, e.g. in therapeutic compositions. They can be used to
CC screen for PRO polypeptide antagonists and agonists useful to identify
CC drug candidates. They can also be used to produce antibodies, useful to
CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
CC therapeutically (e.g. as antagonists or to target and/or deliver
CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
CC produce antisense sequences to inhibit polypeptide production. They can
CC be used to produce probes and primers useful to detect or isolate
CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
CC sequences from other species. They are also useful for gene mapping and
CC to generate transgenic animals. ABS67448-ABS67476 represent human PRO
CC coding sequences, probes and primers of the invention
XX
SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 6; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy         80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy        140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy        200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy        260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy        320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy        380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy        440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

Qy        500 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAG 540

Qy        560 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTCCAGGGATGCATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGG 600

Qy        620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGAC 660

Qy        680 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATAC 720

Qy        740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACT 780

Qy        800 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAA 840

Qy        860 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTCCTATACCCACTTCTGCTC 900

Qy        920 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCA 960

Qy        980 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCCTACCTGTGTGCAGCCCCTTGGAACCTG 1020

Qy       1040 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTATGATGGGTA 1080

Qy       1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

Qy       1160 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200

Qy       1220 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC 1260

Qy       1280 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCC 1320

Qy       1340 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACC 1380

Qy       1400 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCTGTCCATG 1440

Qy       1460 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGA 1500

Qy       1520 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560

Qy       1580 TCTGATAATACAGACCCTGTC 1600
              |||||||||||||||||||||
Db       1561 TCTGATAATACAGACCCTGTC 1581
```

RESULT 14

ABS53475
ID ABS53475 standard; cDNA; 1587 BP.
XX
AC ABS53475;
XX
DT 29-NOV-2002 (first entry)
XX
DE cDNA encoding human PRO1863 polypeptide.
XX
KW Human; secreted and transmembrane polypeptide; PRO polypeptide;
KW T-lymphocyte proliferation; inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; Sjogren's syndrome; thyroiditis;
KW autoimmune haemolytic anaemia; diabetes mellitus; multiple sclerosis;
KW hepatitis; contact dermatitis; allergic disease; psoriasis; virucide;
KW immune related disease; kidney disease; antiinflammatory; antithyroid;
KW antirheumatic; antiarthritic; immunosuppressive; antianaemic;
KW antidiabetic; neuroprotective; hepatotropic; antiinflammatory;
KW dermatological; antiallergic; antipsoriatic; PRO1863; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 17. .1330
FT /*tag= a
FT /product= "PRO1863"
XX
PN US2002098507-A1.
XX
PD 25-JUL-2002.
XX
PF 27-DEC-2001; 2001US-00033326.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2002-673823/72.
DR P-PSDB; ABG31399.
XX
PT Novel PRO polypeptides and nucleic acids encoding the polypeptides,
PT useful for preparing a medicament for the treatment of inflammatory and
PT immune related disorders.
XX
PS Claim 2; Fig 9; 125pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC and transmembrane polypeptides, designated PRO polypeptides, and the
CC polynucleotide sequences encoding them. The PRO polypeptides of the
CC invention include PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917,
CC PRO1868, PRO3434 and PRO1927. The PRO polypeptides can inhibit the
CC stimulation of T-lymphocyte proliferation. The PRO polypeptides are
CC useful for the diagnosis and treatment of inflammatory diseases (e.g.
CC inflammatory bowel disease, rheumatoid arthritis, Sjogren's syndrome,
CC autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus, multiple
CC sclerosis, hepatitis, contact dermatitis, allergic diseases and
CC psoriasis), immune related diseases, and kidney diseases in humans. The
CC present sequence encodes human PRO1863 polypeptide
XX
SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 6; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      20 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCC 60

Qy      80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 120

Qy     140 GTCCGACCTGCCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 199
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTG 180

Qy     200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGG 240

Qy     260 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCACGGAGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCT 300

Qy     320 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCCCTGATCTCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAA 360

Qy     380 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGT 420

Qy     440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGAC 480

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RESULT 15
ADY31901
ID ADY31901 standard; cDNA; 1587 BP.
XX
AC ADY31901;
XX
DT 05-MAY-2005 (first entry)
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DE Novel human secreted and transmembrane protein PRO1181 cDNA.
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KW PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; tumour;
KW cancer; lung; colon; breast; prostate; rectum; liver;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
KW arthritis; sports injury; cytostatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200193983-A1.
XX
PD 13-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017800.
XX
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 20-JUN-2000; 2000US-0212901P.
PR 22-JUN-2000; 2000US-0213807P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-404358/43.
DR P-PSDB; ADY31902.
XX
PT Isolated nucleic acid useful in a method for stimulating the
PT proliferation, gene expression or differentiation of cells and in
PT detecting the presence of a tumor.
XX
PS Claim 2; SEQ ID NO 161; 296pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. They are particularly useful for
CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
CC blood, for stimulating the proliferation or differentiation of
CC chondrocyte cells, for stimulating the proliferation of or gene
CC expression in pericyte cells or for stimulating the proliferation of
CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
CC technology, in generating transgenic animals or knock-out animals which
CC may be used in the development and screening of therapeutically useful
CC reagents, in gene therapy, in chromosome identification, as chromosome
CC markers and in generating probes. The PRO polypeptides, or anti-PRO
CC antibodies, are useful for preparing a medicament for treating a
CC condition which is responsive to the PRO polypeptides or anti-PRO
CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
CC differentiation of chondrocytes. The PRO polypeptides are useful as
CC molecular markers for protein electrophoresis, and in tissue typing. This
CC sequence represents a human PRO polynucleotide of the invention. Note:

CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 7; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Job time : 1054 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:31:52 ; Search time 21 Seconds
(without alignments)
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Perfect score: 2381
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	6.7	28	7	US-11-134-871-3056	Sequence 3056, Ap
2	136	5.7	5738	6	US-10-505-928-150	Sequence 150, App
3	131.5	5.5	1450	7	US-11-217-997-6	Sequence 6, Appli
4	123	5.2	721	7	US-11-175-714-7	Sequence 7, Appli
5	122	5.1	1464	7	US-11-174-307B-2038	Sequence 2038, Ap
6	121.5	5.1	1418	7	US-11-217-997-38	Sequence 38, Appl
7	120.5	5.1	1019	7	US-11-174-307B-334	Sequence 334, App
8	120	5.0	1467	7	US-11-174-307B-1022	Sequence 1022, Ap
9	118.5	5.0	5179	7	US-11-105-233-185	Sequence 185, App
10	118	5.0	251	6	US-10-196-749-476	Sequence 476, App
11	118	5.0	810	7	US-11-174-307B-220	Sequence 220, App
12	117.5	4.9	1868	7	US-11-174-307B-2266	Sequence 2266, Ap
13	116	4.9	1505	7	US-11-174-307B-1622	Sequence 1622, Ap
14	115.5	4.9	1547	7	US-11-217-997-22	Sequence 22, Appl
15	115.5	4.9	1577	7	US-11-217-997-16	Sequence 16, Appl
16	115.5	4.9	1577	7	US-11-217-997-20	Sequence 20, Appl
17	115.5	4.9	1598	7	US-11-174-307B-2072	Sequence 2072, Ap
18	115.5	4.9	1620	7	US-11-217-997-42	Sequence 42, Appl
19	115.5	4.9	1653	7	US-11-217-997-40	Sequence 40, Appl
20	115	4.8	1502	7	US-11-174-307B-632	Sequence 632, App
21	115	4.8	1594	7	US-11-217-997-18	Sequence 18, Appl
22	115	4.8	2133	7	US-11-174-307B-894	Sequence 894, App
23	114.5	4.8	864	7	US-11-178-724-27	Sequence 27, Appl
24	114.5	4.8	1505	7	US-11-174-307B-562	Sequence 562, App
25	114.5	4.8	2003	7	US-11-264-243-8	Sequence 8, Appli
26	114	4.8	717	7	US-11-175-714-9	Sequence 9, Appli
27	114	4.8	2124	7	US-11-174-307B-2768	Sequence 2768, Ap
28	114	4.8	2556	7	US-11-071-796A-22	Sequence 22, Appl
29	113.5	4.8	970	7	US-11-174-307B-2336	Sequence 2336, Ap
30	113.5	4.8	1131	7	US-11-174-307B-2558	Sequence 2558, Ap
31	113.5	4.8	1298	7	US-11-174-307B-2774	Sequence 2774, Ap
32	113.5	4.8	1363	7	US-11-174-307B-358	Sequence 358, App
33	113.5	4.8	1363	7	US-11-174-307B-2430	Sequence 2430, Ap
34	113.5	4.8	1484	7	US-11-174-307B-424	Sequence 424, App
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36	113.5	4.8	1701	7	US-11-174-307B-2440	Sequence 2440, Ap
37	113	4.7	1493	7	US-11-174-307B-4196	Sequence 4196, Ap
38	112.5	4.7	1861	7	US-11-174-307B-2454	Sequence 2454, Ap
39	111.5	4.7	1422	7	US-11-174-307B-690	Sequence 690, App
40	111.5	4.7	1708	7	US-11-174-307B-2136	Sequence 2136, Ap
41	111.5	4.7	1953	7	US-11-264-243-16	Sequence 16, Appl
42	111.5	4.7	2616	7	US-11-174-307B-1680	Sequence 1680, Ap
43	111	4.7	729	7	US-11-175-714-8	Sequence 8, Appli
44	110	4.6	1315	7	US-11-174-307B-610	Sequence 610, App
45	110	4.6	1685	7	US-11-174-307B-2212	Sequence 2212, Ap

ALIGNMENTS

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RESULT 1
US-11-134-871-3056
; Sequence 3056, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
;  APPLICANT: Aebersold, Rudolf H.
;  APPLICANT:  Zhang, Hui
;  TITLE OF INVENTION: Compositions and Methods for
;  TITLE OF INVENTION:  Quatification of Serum Glycoproteins
;  FILE REFERENCE: 66661-116
;  CURRENT APPLICATION NUMBER: US/11/134,871
;  CURRENT FILING DATE:  2005-05-20
;  PRIOR APPLICATION NUMBER: 60/573,593
;  PRIOR FILING DATE: 2004-05-21
;  NUMBER OF SEQ ID NOS: 3602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3056
;   LENGTH: 28
;   TYPE: PRT
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US-11-134-871-3056

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RESULT 2
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; Sequence 150, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 150
;   LENGTH: 5738
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-10-505-928-150

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Db       3300 GSGVRARFRSPSNPPAAWGGAPCEGDRQELQGCHTV-----CGTGIAGSLGAGVPPSSSQ 3354

Qy         83 EPRVTEHRMGP------GLSLISYT-----FVCRQEDFCNNLVNSLPLWAPQPP--ADPG 129
                 :  | |||      |: :  :|       | |            | |  :      ||
Db       3355 FCTLRTHGMGPTDHSTWGIEVFGWTPWTSWSSCSQSCLA---PGGGPGWRSRSRLCPSPG 3411

Qy        130 SLRCPVCLSMEGCLEGTTEE----------ICPKGTTHCYDGLLRLRGGGIFSNLRVQGC 179
               ||         : | ||           |  | | |  ||           |     |
Db       3412 DSSCPG--------DATQEEPCSPPIECTGFCAPGCT-CPPGLF----------LHNASC 3452

Qy        180 MP--QPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGN--LAQEPTDWTTSNT 235
              :|  |  | |       | :   ::||     ||  |    |     :|  : ||  :
Db       3453 LPRSQCPCQLHGQLYASGAMARLDSCNN---CTCVSGKMACTSERCPVACGWSPWTLWSL 3509

Qy        236 EMCEVGQVCQETLLLIDVGLTSTL-VGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFC 294
               |              :||:      ||   :  |    |  |: :             ||
Db       3510 CSCS-----------CNVGIRRRFRAGTAPPAAFGGAECQGPTMEA-----------EFC 3547

Qy        295 SSDLCNSASSSSVLLNSLPPQAAPVPG----DRQCPTCVQPLGTCSSGSPRMTCPRGATH 350
                          || |  ||||    |:|   | |  :|:       :: |||
Db       3548 ---------------SLRPCPGPVPGMCPRDKQWLDCAQGPASCA----ELSAPRGTNQ 3587

Qy        351 -CYDGYIHLSGGGLSTKMSIQGCVAQPSSFLL-----NHTRQIGIFSAREKRDVQPPASQ 404
               |:                  ||   ||  ||     |   :|         ||||  :
Db       3588 TCH-----------------PGCHC-PSGMLLLVSPRGHPGPLG-------ASVQPPVAL 3622

Qy        405 HEGGGAEGLESLT----WGVGLALAPALW--WGVVCPSC 437
                 || |  |:     ||          | |      ||
Db       3623 ---PGAIGTGSVPGAGGWGP--------WGPWSHCSRSC 3650


RESULT 3
US-11-217-997-6
; Sequence 6, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
;  APPLICANT: Valerie L. Gerlach
;  APPLICANT:  Elma R. Fernandes
;  APPLICANT:  Richard A. Shimkets
;  APPLICANT:  Meera Patturajan
;  APPLICANT:  Vladimir Y. Gusev
;  APPLICANT:  Stacie (Casman) Navara
;  APPLICANT:  Velizar T. Tchernev
;  APPLICANT:  David W. Anderson
;  APPLICANT:  Xiaojia (Sasha) Guo
;  APPLICANT:  Luca Rastelli
;  APPLICANT:  Mei Zhong
;  APPLICANT:  Muralidhara Padigaru
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
;  FILE REFERENCE: Cura 551 CIP
;  CURRENT APPLICATION NUMBER: US/11/217,997
;  CURRENT FILING DATE:  2005-08-31
;  PRIOR APPLICATION NUMBER: 10/453,372
;  PRIOR FILING DATE: 2003-06-03
;  PRIOR APPLICATION NUMBER: 10/055,877
;  PRIOR FILING DATE: 2002-01-22
;  PRIOR APPLICATION NUMBER: 60/262,892
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,598
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/263,799
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/264,117
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,139
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,478
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/263,351
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/272,870
;  PRIOR FILING DATE: 2001-03-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
;   LENGTH: 1450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-217-997-6

  Query Match             5.5%;  Score 131.5;  DB 7;  Length 1450;
  Best Local Similarity   22.7%;  Pred. No. 0.0052;
  Matches  116;  Conservative   34;  Mismatches  212;  Indels  149;  Gaps   31;

Qy          5 LLLALLGFILPL----------PGVQALL-CQFGTV-QHVWKVSDLPRQWTPKNTSCDS 51
              | |   |:: |            || : |  || |    ||      | |  : | ||:
Db        884 LCLCEAGYVGPRCEQQCPQGHFGPGCEQLCQCQHGAACDHVSGACTCPAGW--RGTFCEH 941

Qy         52 -------GLGCQDTLMLIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVC 104
                     || |:       :|      |       | : || |   |     ||   |  |
Db        942 ACPAGFFGLDCRSACN-CTAGAACDAVNGSCLCPAGRRGPRCAE-TCPAGL----YGDNC 995

Qy        105 RQEDFCNNLVNSLPL---------WA------PQPPADPGSLRCPVCLSMEGCLEG---- 145
              |    | |      |:         ||        || |  :     |    ||| |
Db        996 RHSCLCQNGGTCDPVSGHCACPEGWAGLACEKECPPRDVRA----GCRHSGGCLNGGLCD 1051

Qy        146 --TTEEICPKGTT--HCYDGLLRLRGGGIFSNLRVQGCMPQPGCNLLNGTQEIGPVGMTE 201
                  |  :|| |      |    ||    | |      | |   ||
Db       1052 PHTGRCLCPAGWAGDKCQSPCLR----GWFGEACAQHCSCPPGA---------------- 1091

Qy        202 NCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEM-CEVGQV---CQETLLLIDVGLTS 257
                       || |          :  | :| |  |  |  |:    |::    :: |
Db       1092 --------ACHHVT------GACRCPPGFTGSGCEQGCPPGRYGPGCEQLCGCLNGGSCD 1137

Qy        258 TLVGTKGCST--VGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNS--LP 313
                 |  | |  :|   :      : | |    : || |    |   ::   :  :   |
Db       1138 AATGACRCPTGFGLTDCNL-----TCPQGRFGPNCTHVCG---CGQGAACDPVTGTCLCP 1189

Qy        314 PQAAPVPGDRQCP----------TC-VQPLGTCSSGSPRMTCPRGAT--HC--------Y 352
              |  | |  :| ||          ||  :  | | : :   :|  | |  ||         |
Db       1190 PGRAGVRCERGCPQNRFGVGCEHTCSCRNGGLCHASNGSCSCGLGWTGRHCELACPPGRY 1249

Qy        353 DGYIHL--SGGGLSTKMSIQG-CVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGG 409
                 ||  |    ||     | | |    |          |  :     ||    | |
Db       1250 GAACHLECSCHNNSTGEPATGTCRCGPG-----------FYGQACEHPCPPG--FHGAG 1295

Qy        410 AEGLESLTWGV------GLALAPALWWGVVC 434
                :||      |       | | || : | |
Db       1296 CQGLCWCQHGAPCDPISGRCLCPAGFHGHFC 1326


RESULT 4
US-11-175-714-7
; Sequence 7, Application US/11175714
; Publication No. US20060122373A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  McCarthy, Sean A.
;  APPLICANT:  Gearing, David
;  APPLICANT:  Holtzman, Douglas A.
;  APPLICANT:  Pan, Yang
;  APPLICANT:  Busfield, Samantha J.
```

```
;  APPLICANT:  Barnes, Thomas M.
;  APPLICANT:  Mackay, Charles
;  APPLICANT:  Lora, Jose M.
;  TITLE OF INVENTION: DELTA3, FTHMA-070, TANGO85, TANGO77,
;  TITLE OF INVENTION:  SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN
;  TITLE OF INVENTION:  AND NUCLEIC ACID MOLECULES AND USES THEREOF
;  FILE REFERENCE: MPI05-010OMNIM
;  CURRENT APPLICATION NUMBER: US/11/175,714
;  CURRENT FILING DATE:  2005-07-05
;  PRIOR APPLICATION NUMBER: US 10/417,719
;  PRIOR FILING DATE: 2003-04-17
;  PRIOR APPLICATION NUMBER: US 09/568,218
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 09/872,855
;  PRIOR FILING DATE: 1997-06-11
;  PRIOR APPLICATION NUMBER: US 09/832,633
;  PRIOR FILING DATE: 1997-04-04
;  PRIOR APPLICATION NUMBER: US 10/895,676
;  PRIOR FILING DATE: 2004-07-21
;  PRIOR APPLICATION NUMBER: US 10/105,934
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: US 09/862,972
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 09/062,389
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: US 60/062,017
;  PRIOR FILING DATE: 1997-10-10
;  PRIOR APPLICATION NUMBER: US 60/044,746
;  PRIOR FILING DATE: 1997-04-18
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 195
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 721
;   TYPE: PRT
;   ORGANISM: Xenopus Laevis
US-11-175-714-7

  Query Match             5.2%;  Score 123;  DB 7;  Length 721;
  Best Local Similarity   23.2%;  Pred. No. 0.012;
  Matches   84;  Conservative   22;  Mismatches  126;  Indels  130;  Gaps   21;

Qy         99 SYTFVCRQ-------EDFC---------------NNLVNSLPLWAP--------QPPAD 127
              || |||  :        |:|                ||  |   |  |          |   |
Db        176 SYRFVCDEYYYGEGCSDYCRPRDDAFGHFSCGEKGENLCN--PGWKGLYCTEPICLPGCD 233

Qy        128 --------PGSLRCPV---------CLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGI 170
                      || :| |          |:   ||| || ::        :| :|        ||:
Db        234 EHHGYCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQ---PWQCNCQEG-----WGGL 285

Qy        171 FSNLRVQGCMPQPGCNLLNG-----------TQEIGPVGMTENC----NRKDFLTCHRGT 215
              | |  :  |   |    ||              |     |    ||    |  |  |   |
Db        286 FCNQDLNYCTHHKPCE--NGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDANPCKNGG 343

Qy        216 TIMTHGNLAQEPTDWTTSNTEMCE---VGQVCQETLLLIDVGLTSTLVGTKGCSTVG--A 270
               :          :|   | |  |      |: |:          |::      |   |  |
Db        344 SC----------SDLENSYTCSCPPGFYGKNCE---------LSAMTCADGPCFNGGRCA 384

Qy        271 QNSQKTTIHSAPPGVLVASYTHF--------CSSDLCNSASSSSVLLNSLPPQAAPVPGD 322
                |    |   | |    |: |        |||: | : :      | ||  |
Db        385 DNPDGGYICPCPVG-----YSGFNCEKKIDYCSSNPCANGARCEDLGNSYICQCQEGFSG 439

Qy        323 RQC----PTCV----QPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVA 374
              | |     |      | ||| |    :|      |  |||       | :  | |  |
Db        440 RNCDDNLDDCTSFPCQNGGTCQDGINDYSCT-----CPPGYI-----GKNCSMPITKCEH 489

Qy        375 QP 376
               |
Db        490 NP 491

RESULT 5
US-11-174-307B-2038
; Sequence 2038, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2038
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: PFam Name: zf-TRAF; PFam Description: TRAF-type zinc finger
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 21593788; NR Description: unknown [Arabidopsis thali
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 50939745; NR Description: XIAP associated
;   OTHER INFORMATION: factor-1-like protein [Oryza sativa (japonica cultivar-group)]
;   OTHER INFORMATION: >gi|33354198|dbj|BAC81156.1| XIAP associated factor-1-like prot
;   OTHER INFORMATION: [Oryza sativa (japonica cultivar-group)] [Oryza sativa (japonic
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 49114926; NR Description: MGC80116 protein
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 34872552; NR Description: similar to FLN29 gene
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 50756455; NR Description: PREDICTED: similar to
US-11-174-307B-2038

  Query Match             5.1%;  Score 122;  DB 7;  Length 1464;
  Best Local Similarity   21.3%;  Pred. No. 0.033;
  Matches   76;  Conservative   18;  Mismatches  156;  Indels  106;  Gaps   14;

Qy        141 GCLEGTTEEICPKGTTHCY------DGLLRLRGGGIFSNLRVQGCMPQPGCN-------- 186
              ||    |      ||  |          |       |||   :      |     ||
Db        354 GCATAATGGTTGTATTTCTCCTGAGGGACTTTGGGATTCACTCGTTAAAGCTGGGATTGA 413

Qy        187 ----LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQ 242
                        |     |   |  |  |        ||  |||     |  |     |  |  |  |
Db        414 GATAAAAGATGAGGAGCTTGC------TC--GTTTTGTGGAA-----CATGTTGACAAGG 460

Qy        243 VCQET-----LLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSD 297
                |  |                |   |   |   |  :| ||    ||    :      :  |  :
Db        461 ACAATGATGGAATCATTATGTTTGAAGAATGGAGAGATTTTCTTTTG---CTGTACCCTC 517

Qy        298 LCNSASSSSVLLNSLPPQAAPVPGDRQCPTCV-----------QPLGTCSSGSPRMTCPR 346
                | :|   ::      :      ||                            |||::|:     |
Db        518 ACGAAGCTACCATT-GAAAATATATACCATCACTGGGAAAGAGTATGTCTTGTAGATATT 576

Qy        347 G-------------ATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSA 392
              |              || |  |     : || :|      || |   ::
Db        577 GGAGAACAAGCTGTAATTCCAG----AAGGCAT---CAGCAAACAT------------- 615
```

```
Qy        393 REKRDVQPPASQHEGGGAEGLESLT----------WGVGLALAPALWWGVVCPSC 437
Db        616 ---------ATAAAGAGGAGTAACTATTTCATCGCAGGTGGCATAGCTGGTGCAGC 662
```

RESULT 6
US-11-217-997-38
; Sequence 38, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shimkets
; APPLICANT: Meera Patturajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchernev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 38
; LENGTH: 1418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-38

Query Match 5.1%; Score 121.5; DB 7; Length 1418;
Best Local Similarity 23.1%; Pred. No. 0.035;
Matches 126; Conservative 33; Mismatches 185; Indels 201; Gaps 37;

```
Qy          5 LLLALLGFILPL-----------PGVQALL-CQFGTV-QHVWKVSDLPRQWTPKNTSCDS 51
Db        892 LCLCEAGYVGPRCEQQCPQGHFGPGCEQLCQCQHGAACDHVSGACTCPAGW--RGTFCEH 949

Qy         52 -------GLGCQDTLMLIESGPQVSLVLSKGCTEAKDQEPRVTEH------RMGPGLSLI 98
Db        950 ACPAGFFGLDCRSACN-CTAGAACDAVNGSCLCPAGRRGPRCAEKCLPRDVRAG------ 1002

Qy         99 SYTFVCRQEDFCNNLVNSLPLWAPQPPADP--GSLRCPV------CLSMEGCLEGTTEEI 150
Db       1003 -----CRHSGGCLN--GGL--------CDPHTGRCLCPAGWTGDKCQS--PCLRGWFGEA 1045

Qy        151 C-------PKGTTHCYDGLLRLRGGGIFSNLRVQGCMP---QPGCNLLNGTQEIG----- 195
```

```
Db       1046 CAQRCSCPPGAACHHVTGACRCPPGFTGSGCE-QGCPPGRYGPGCEQLCGCLNGGSCDAA 1104

Qy        196 ------PVG-MTENCNRKDFLTCHRG------TTIMTHG-NLAQEPTDWTTSNTEMCEVG 241
Db       1105 TGACRCPTGFLGTDCN----LTCPQGRFGPNCTHVCGCGQGAACDP----VTGTCLCPPG 1156

Qy        242 QV----------------CQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGV 285
Db       1157 RAGVRCERGCPQNRFGVGCEHTCSCRNGGLCHASNGSCSC---GLGWTGRHCELACPPGR 1213

Qy        286 LVASYTHFCS---SDLCNSASSSSVLLNSLPPQAAPVPGDRQCPT------CVQPLGTCS 336
Db       1214 YGAACHLECSCHNNSTCEPATGTCRCGPGFYGQACEHP----CPPGFHGAGC-QGLCWCQ 1268

Qy        337 SGSP------RMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIF 390
Db       1269 HGAPCDPISGRCLCPAG----FHGH-----------FCERGC--EPGSF----------- 1300

Qy        391 SAREKRDVQPPASQHEG--------GGAEGLESLTWGVGLALAPALWWGVVC-------- 434
Db       1301 --------------GEGCHQRCDCDGGAP-CDPVT---GLCLCPPGRSGATCNLDCRRGQ 1342

Qy        435 --PSC 437
Db       1343 FGPSC 1347
```

RESULT 7
US-11-174-307B-334
; Sequence 334, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 334
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: PFam Name: Man-6-P_recep; PFam Description: Cation-dependent
US-11-174-307B-334

Query Match 5.1%; Score 120.5; DB 7; Length 1019;
Best Local Similarity 24.6%; Pred. No. 0.029;
Matches 68; Conservative 13; Mismatches 140; Indels 55; Gaps 12;

```
Qy        133 CPVCLSMEGCLEGTTEEICP-----KGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCNL 187
Db        438 CATCCT--GCCGGTTGTGCAGTAGCTATATCCGGCCATAG-----TAGTGGATGGGGCT- 489

Qy        188 LNGTQEIGPVGMTENCNRKDFLT---------CHRGTTIMTHGNLAQEPTDWTTSNTEMC 238
Db        490 -GGTTTAGTACCTTACTAATCATTATCTTGTGCCTGTTTGGAGCTTATCTGGTGGGTG-- 546

Qy        239 EVGQVCQET-------------LLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGV 285
Db        547 --GTGCAGTATATCGGTATTTCTCCCTTGGAATTCGTGGCATAGATGTAATCCCGAATG- 603
```

```
Qy        286 LVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLG-TCSSGSPRMTC 344
                  | |:  | : : ::    :    |    |   | |    | ||:  :   ||
Db        604 -TGGATTACTGGGCCACTGTACCTCACAGTATACAG-AGCTTTTTGGCTCACTATTTC 661

Qy        345 PRGATHCYDGYIHLSGGG------LSTKMSIQGCVA 374
                |||  |  |    |||          |  :  || |
Db        662 AAGATTCGGG-----GGGTCTAGTCGTGGTCAGCAA 692

RESULT 8
US-11-174-307B-1022
; Sequence 1022, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 1022
;   LENGTH: 1467
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: PFam Name: Aa_trans; PFam Description: Transmembrane amino
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 34912776; NR Description: P0407B12.25 [Oryza
;   OTHER INFORMATION: sativa (japonica cultivar-group)] >gi|11034686|dbj|BAB17188.1|
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 21554158; NR Description: amino acid permease-like
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 22136372; NR Description: amino acid permease-like
;   OTHER INFORMATION: protein [Arabidopsis thaliana] >gi|20466438|gb|AAM20536.1| amino
;   OTHER INFORMATION: acid permease-like protein [Arabidopsis thaliana]
;   OTHER INFORMATION: >gi|18422139|ref|NP_568597.1| amino acid transporter family prote
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 10177364; NR Description: amino acid permease-like
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 50932903; NR Description: putative amino acid
;   OTHER INFORMATION: transporter family II [Oryza sativa (japonica cultivar-group)]
;   OTHER INFORMATION: >gi|48475084|gb|AAT44153.1| putative amino acid transporter famil
US-11-174-307B-1022

  Query Match             5.0%;  Score 120;  DB 7;  Length 1467;
  Best Local Similarity   21.6%;  Pred. No. 0.049;
  Matches   74;  Conservative   16;  Mismatches  136;  Indels  116;  Gaps   14;

Qy        129 GSLRCPVC--LSMEGCLE--GTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPG 184
                |:  |  |   :  ||    | |   |    ||| |   |       |||           |
Db        554 GTCTCTGCTTCTCAGCTTAGGATATACT--TTCCTCGTCGTTGGG-------------G 597

Qy        185 CNLLNGTQEIGPVGMTENCNRKDFLTCHR-----GTTIMTHGNLAQE----------PT 228
                |     ||                      ||    |||    |  |          |
Db        598 CT--TGT----------------ATCAACCTAGGTTTGTCGAAAAACGCTCCTAAACGT 638

Qy        229 DWTTSNTEMCEVGQVCQETLLLID--------VGLTSTLVGTKGCSTVGAQNSQKTTIHS 280
                |: |   |   |  |   |              | |:|  ||  |:|          ||
Db        639 GAGTATTCTCTAGAGCATTCGGATTCAGGGAAAGTTTTAGTGCCTTCACATCAATTTCG 698

Qy        281 APPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQAAPVPGDRQCPT---CVQPLGTCSS 337
                |              |::  |   ::::         ||   |   |   |     |:
Db        699 AT-----------CATAGCTGCTATTTTCGG----AAATGGAATCTTACCCGAAATACAG 743

Qy        338 GSPRMTCPRGAT--HCYDGYIHLSGGGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREK 395
                |    ||  |  |   |   |       :|||  :         |   |
Db        744 GCAACTCTTGCTCCACCAGCCACAGGGAAGATGTTGAAA-------------------- 782

Qy        396 RDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC 437
                             |||     :  |  |  |         |   |  :|
Db        783 ------------GGACTATTGTTGTGTTATAGTGTGATCTTC 812

RESULT 9
US-11-105-233-185
; Sequence 185, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
;  APPLICANT: Thiagalingam et al
;  TITLE OF INVENTION: Differential Expression of Genes in MSI
;  TITLE OF INVENTION:  Tumors
;  FILE REFERENCE: 1657/2001
;  CURRENT APPLICATION NUMBER: US/11/105,233
;  CURRENT FILING DATE:  2005-04-13
;  NUMBER OF SEQ ID NOS: 202
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 185
;   LENGTH: 5179
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-105-233-185

  Query Match             5.0%;  Score 118.5;  DB 7;  Length 5179;
  Best Local Similarity   20.2%;  Pred. No. 0.29;
  Matches   81;  Conservative   48;  Mismatches  123;  Indels  149;  Gaps   24;

Qy         96 SLISYTFVCRQEDFC----NNLVNSLPLWAPQ-------PPADPGSLRCPVCLS------ 138
                || :|  :| |:: |      |:     :    :          ||:          | | |
Db       4733 SLQAYAALCAQQNICLDWRNHTHGACLVECPSHREYQACGPAEE-----PTCKSSSSQQN 4787

Qy        139 ----MEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGC-------MPQ----- 182
                    :|||        ||:||  :    |              :: |: |          :|:
Db       4788 NTVLVEGC-------FCPEGTMNYAPGF---------DVCVKTCGCVGPDNVPREFGEH 4830

Qy        183 -----PGCNLLNGTQEIGPVGMTENCNRKDFLTC-HRGTTIMTHGNLAQEPTDWTTSNTE 236
                       |  ||    | :    : |::|    |    || :  |    |    | | |  |
Db       4831 FEFDCKNCVCLEGGS--GIICQPKRCSQKPVTHCVEDGTYLATEVN----PAD-TCCNIT 4883

Qy        237 MCEVG-QVCQETLLLIDVG--LTSTLVGTKGCSTVGAQNSQKTTIH---SAPPGVLVASY 290
                :|:      :|:|   :   :|   :  | :|  |          : |:    :|    || |  |
Db       4884 VCKCNTSLCKEKPSVCPLGFEVKSKMVPGRCCPFYWCE-SKGVCVHGNAEYQPGSPV--Y 4940

Qy        291 THFCSSDLCNSASSSSVLLNSLPPQAAP------------VPGDRQCPTCVQ------- 330
                :   |    :|      :: |||  :         |         ||:   |   |
Db       4941 SSKCQDCVCTDKVDNNTLLNVIACTHVPCNTSCSPGFELMEAPGE-CCKKCEQTHCIIKR 4999

Qy        331 ----------------PLGTCS------------SGSPRMTCPR-GATHCYDGYIHLSGG 361
                                  |    |:                |    :|||    |:  |   ||
Db       5000 PDNQHVILKPGDFKSDPKNNCTFFSCVKIHNQLISSVSNITCPNFDASICIPGSITFMPN 5059

Qy        362 G------------------LSTKMSIQGCVAQPSSFLLNH 383
                |                    ::|::|   ||        :  |:||
Db       5060 GCCKTCTPRNETRVPCSTVPVTTEVSYAGCT---KTVLMNH 5097

RESULT 10
```

```
US-10-196-749-476
; Sequence 476, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C340
;  CURRENT APPLICATION NUMBER: US/10/196,749
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 476
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-196-749-476

  Query Match             5.0%;  Score 118;  DB 6;  Length 251;
  Best Local Similarity   25.2%;  Pred. No. 0.0087;
  Matches   57;  Conservative   37;  Mismatches   92;  Indels   40;  Gaps   16;

Qy          4 VLLLALLGFILPLPGVQALLCQFGTVQHVW------KVSDLPRQWTPKNTSCDSGLGCQD 57
              |:|| | |  | | | ||| |   : :| :      :   ||      : ||     | :
Db          8 VILLCLFGAALCLTGSQALQCY--SFEHTYFGPFDLRAMKLP------SISCPH--ECFE 57

Qy         58 TLMLIESGPQVSLVL-SKGCTEAKDQEPRVTEHRMGPGLSLISYTFV--CRQEDFCN-NL 113
               :: :::| :  : |  |||       |   : :  |      |: |  |   | || :|
Db         58 AILSLDTGYRAPVTLVRKGCWTG----PPAGQTQSNPDALPPDYSVVRGC-TTDKCNAHL 112

Qy        114 V--NSLP--LWAPQPPADPGSLRCPVCLSM--EGCLEGTTEEI-CPKGTTHCYDGLLRLR 166
              :  ::||    || ||   |:  |  |: :  : |  | :  : | :  | |: |  |:
Db        113 MTHDALPNLSQAPDPPTLSGA-ECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMT 171

Qy        167 GGGIFSNLRVQGCMPQPGCNLLNGTQEIGPVGMTEN------CNRK 206
                |     : :: |  :| |      |      : :  :      ||||
Db        172 VGNFSVPVYIRTC-HRPSCTTEGTTSPWTAIDLQGSCCEGYLCNRK 216


RESULT 11
US-11-174-307B-220
; Sequence 220, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 220
;   LENGTH: 810
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-11-174-307B-220

  Query Match             5.0%;  Score 118;  DB 7;  Length 810;
  Best Local Similarity   25.8%;  Pred. No. 0.035;
  Matches   68;  Conservative   14;  Mismatches  130;  Indels   52;  Gaps   13;

Qy        133 CPVCLSMEGCLEGTTEEICP-----KGTTHCYDGLLRLRG----GGIFSNLRVQG---CM 180
              |  | :  ||  |||   |          |  |  |      |    ||         |   |
Db        550 CATCCT--GCCGGTTGTGCAGCAGCTATATCCGGCCATAGTAGTGGATGGGGCTGTATCT 607

Qy        181 PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHG----NLAQEPTDWTTSNTE 236
                ||    ||   |  | |           ||  ||   | |    |       |  : |
Db        608 TGTGC--CTGT-TTGGAGCTT-------ATCTGGTGGGTGGTGCAGTATATCGGTATTTC 657

Qy        237 MCEVGQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSS 296
                |     |  |       |  :|  || ||:| ||  :  |    |         |  |:
Db        658 TC-----CCTT------GGAATTCGTGGCATAGATGTAATCCCGA--ATATGGATTACTG 704

Qy        297 DLCNSASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYI 356
                | : : ::    :    |    |      |       ||:  :   ||  |||  |  |
Db        705 GGCCACTGTACCTCACAGTATACAGAGCTGTTTTGGCTCACTATTTTCAAGATTCGGG-- 762

Qy        357 HLSGGGLSTKM------SIQGCVA 374
                |||  |         :  || |
Db        763 ---GGGTCTATTCGTGGTCAGCAA 783


RESULT 12
US-11-174-307B-2266
; Sequence 2266, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2266
;   LENGTH: 1868
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: PFam Name: Glyco_hydro_17; PFam Description: Glycosyl
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: PFam Name: X8; PFam Description: X8 domain
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 7270016; NR Description: 1, 3-beta-glucanase-like
;   OTHER INFORMATION: protein [Arabidopsis thaliana] >gi|38257777|sp|Q9M088|E135_ARATH
;   OTHER INFORMATION: Putative glucan endo-1,3-beta-glucosidase 5 precursor
;   OTHER INFORMATION: ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 23308419; NR Description: At5g58090/k21l19_70
;   OTHER INFORMATION: [Arabidopsis thaliana] >gi|16604491|gb|AAL24251.1|
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 9759535; NR Description: glucanase; glucan
;   OTHER INFORMATION: endo-1,3-beta-glucosidase [Arabidopsis thaliana]
;   OTHER INFORMATION: >gi|38257732|sp|Q93Z08|E136_ARATH Putative glucan
;   OTHER INFORMATION: endo-1,3-beta-glucosidase 6 precursor ((1->3)-beta-glucan
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 15242078; NR Description: glycosyl hydrolase
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 50921029; NR Description: putative
;   OTHER INFORMATION: 1,3-beta-glucanase [Oryza sativa (japonica cultivar-group)]
;   OTHER INFORMATION: >gi|30017525|gb|AAP12947.1| putative 1,3-beta-glucanase [Oryza
US-11-174-307B-2266

  Query Match             4.9%;  Score 117.5;  DB 7;  Length 1868;
  Best Local Similarity   24.5%;  Pred. No. 0.11;
  Matches   61;  Conservative   12;  Mismatches  155;  Indels   21;  Gaps    9;

Qy        133 CPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCNL----- 187
              |.| :  ||   |    |  | | |         |||        ||   ||
Db       1424 CGCCAAATGCTAATC-TTCAGGATCC--TCAGTTGGGACC---AAGCGTGAGCTACGCTT 1477

Qy        188 -LNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQE 246
               |   |  | | |      || | |  | |     | |       |       |
Db       1478 GTGATCATGCTGATTGC-ACCAGTCTTGGTTATGGCTCCTCTTGTGGTAACCTGAATCTA 1536

Qy        247 TLLLIDVGLTSTLVGT-KGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSS 305
                  :|  ||  || | |  | : |   :   |   |     |:  | : : :
Db       1537 GCACAGAATGTTTCGTATGCGTTCAATAGCTATTACCAGGTAAGTAATCAGCTCGACAGT 1596

Qy        306 SVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLST 365
              :          |      ||    |||:  :   |   ||| |       :|||  |
Db       1597 GCGTGTAAGTTCCCGGGTCTCTCTATAGTCAGTA--CTAGGGAT-CCTTCTGTTGGGAGT 1653

Qy        366 KMSIQGCVA 374
                || |
Db       1654 ----TGCAA 1658


RESULT 13
US-11-174-307B-1622
; Sequence 1622, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 1622
;   LENGTH: 1505
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 34905882; NR Description: P0458E05.17 [Oryza
;   OTHER INFORMATION: sativa (japonica cultivar-group)] >gi|21902069|dbj|BAC05617.1|
US-11-174-307B-1622

  Query Match             4.9%;  Score 116;  DB 7;  Length 1505;
  Best Local Similarity   24.2%;  Pred. No. 0.11;
  Matches   72;  Conservative   17;  Mismatches  138;  Indels   70;  Gaps   14;

Qy        129 GSLRCPVCLSMEGCLEGTTEEICPKG-TTHCYDGLLRLRG--GGIFSNLRVQG------- 178
              |: |    :   |   ||   | | ||     |      |  ||  :     |
Db        330 GAAACTCTCACTTCCAATTTCTCTAGATTGATTGGTTCTGGTGGCTATAGCAGTATCTAC 389

Qy        179 -----------CMPQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEP 227
                        |   ||     |  | | | |      ||  ||| | | |
Db        390 ATGGCTCGCTTCTCTGGCTCTGATAAAGCGGCTCTC-AAGGTTCATGTTAGTAGTCACCG 448

Qy        228 TDWT---------TSNTEMCEVGQVCQETLLLIDVGLTSTLVGTKGCSTVG-----AQNS 273
              | |         |:    | | |         | |:|   | ||:| |     | :
Db        449 TCTTTATCAAGTCTTTAGACTTGAGC-------TTGATATT--TTGCTTCGTCTTCAACA 499

Qy        274 QKTTIHSAPPGVLVASYTHFCSSDLCNS----ASSSSVLLNSLPPQAAPVPGD----RQC 325
              |  | |  |  | | |::  | :    :: :         ||  |       |
Db        500 TCCTAACATTGTCAAGCT-TCTTGGCTATTTCGATGATTCAGAGGAAAATGGTGCTCTTC 558

Qy        326 PTCVQPLG--------TCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVA 374
              ||    |        ||::|   ||    | |  |     :|    |  :  || |
Db        559 TTCTTGAGTATCTTCCTCAAGGAAATC----TACAAG----AGAAGCTCCAAAGCAA 607


RESULT 14
US-11-217-997-22
; Sequence 22, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
;  APPLICANT: Valerie L. Gerlach
;  APPLICANT:  Elma R. Fernandes
;  APPLICANT:  Richard A. Shimkets
;  APPLICANT:  Meera Patturajan
;  APPLICANT:  Vladimir Y. Gusev
;  APPLICANT:  Stacie (Casman) Navara
;  APPLICANT:  Velizar T. Tchernev
;  APPLICANT:  David W. Anderson
;  APPLICANT:  Xiaojia (Sasha) Guo
;  APPLICANT:  Luca Rastelli
;  APPLICANT:  Mei Zhong
;  APPLICANT:  Muralidhara Padigaru
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
;  FILE REFERENCE: Cura 551 CIP
;  CURRENT APPLICATION NUMBER: US/11/217,997
;  CURRENT FILING DATE:  2005-08-31
;  PRIOR APPLICATION NUMBER: 10/453,372
;  PRIOR FILING DATE: 2003-06-03
;  PRIOR APPLICATION NUMBER: 10/055,877
;  PRIOR FILING DATE: 2002-01-22
;  PRIOR APPLICATION NUMBER: 60/262,892
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,598
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/263,799
;  PRIOR FILING DATE: 2001-01-24
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;  PRIOR APPLICATION NUMBER: 60/264,117
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,139
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,478
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/263,351
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/272,870
;  PRIOR FILING DATE: 2001-03-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 22
;   LENGTH: 1547
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-217-997-22

  Query Match             4.9%;  Score 115.5;  DB 7;  Length 1547;
  Best Local Similarity   20.6%;  Pred. No. 0.12;
  Matches  124;  Conservative   36;  Mismatches  210;  Indels  231;  Gaps   35;

Qy         17 PGV-QALLCQFGTV-QHVWKVSDLPRQWTPKNTSCDS-------GLGCQDTLMLIESGPQ 67
              ||  |   || |    ||      |  |  : | |:        || |:       :|
Db        887 PGCEQRCQCQHGAACDHVSGACTCPAGW--RGTFCEHACPAGFFGLDCRSACN-CTAGAA 943

Qy         68 VSLVLSKGCTEAKDQEPRVTE---------HR-------------------------MG 92
                |       |  : ||  |         |                          ||
Db        944 CDAVNGSCLCPAGRRGPRCAESACPAHTYGHNCSQACACFNGASCDPVHGQCHCAPGWMG 1003

Qy         93 P--------GLSLISYTFVCRQEDFCNNLVNSLPL---------WAPQPPADPGSLRCPV 135
              |        ||    |   ||    | |     |:         ||          | | |
Db       1004 PSCLQACPAGL----YGDNCRHSCLCQNGGTCDPVSGHCACPEGWA--------GLACEV 1051

Qy        136 ----------CLSMEGCLEG------TTEEICPKGTT-----------------HCYDGL 162
                       |    ||| |      |   :|| | |                 || :|
Db       1052 ECLPRDVRAGCRHSGGCLNGGLCDPHTGRCLCPAGWTGDKCQSPAACAKGTFGPHC-EGR 1110

Qy        163 LRLRGG--------------------------GIFSNLRVQGCMPQPG--CNLLNGT-- 191
                | |                         | |     | |   ||  |: : |
Db       1111 CACRWGGPCHLATGACLCPPGWRGPHLSAACLRGWFGEACAQRCSCPPGAACHHVTGACR 1170

Qy        192 -----------QEIGPVGMTENCNRK-----DFLTCHRGTTIMT-----HGNLAQEPTDW 230
                        |    |    |:| :      :   ||  |   :     ||   |
Db       1171 CPPGFTGSGCEQACPPGSFGEDCAQMCQCPGENPACHPATGTCSCAAGYHGPSCQ----- 1225

Qy        231 TTSNTEMCEVGQV---CQETLLLIDVGLTSTLVGTKGCST--VGAQNSQKTTIHSAPPGV 285
                 : |  |:    |::    :: |      |   | |  :|  :      : | |
Db       1226 -----QRCPPGRYGPGCEQLCGCLNGGSCDAATGACRCPTGFLGTDCNL-----TCPQGR 1275

Qy        286 LVASYTHFCSSDLCNSASSSSVLLNS--LPPQAAPVPGDRQCP----------TC-VQPL 332
                : || |    |   ::   :  :   || | |  :| ||           ||  :
Db       1276 FGPNCTHVCG---CGQGAACDPVTGTCLCPPGRAGVRCERGCPQNRFGVGCEHTCSCRNG 1332

Qy        333 GTCSSGSPRMTCPRGAT--HC--------YDGYIHL--SGGGLSTKMSIQG-CVAQPSSF 379
              | | : :   :|  | |  ||        |    ||  |    ||     | |   |
Db       1333 GLCHASNGSCSCGLGWTGRHCELACPPGRYGAACHLECSCHNNSTCEPATGTCRCGPG-- 1390

Qy        380 LLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV------GLALAPALWWGVV 433
                    |  :      ||     | | :||      |       |  | || : |
Db       1391 ----------FYGQACEHPCPPG--FHGAGCQGLCWCQHGAPCDPISGRCLCPAGFHGHF 1438

Qy        434 C 434
              |
Db       1439 C 1439


RESULT 15
US-11-217-997-16
; Sequence 16, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
;  APPLICANT: Valerie L. Gerlach
;  APPLICANT:  Elma R. Fernandes
;  APPLICANT:  Richard A. Shimkets
;  APPLICANT:  Meera Patturajan
;  APPLICANT:  Vladimir Y. Gusev
;  APPLICANT:  Stacie (Casman) Navara
;  APPLICANT:  Velizar T. Tchernev
;  APPLICANT:  David W. Anderson
;  APPLICANT:  Xiaojia (Sasha) Guo
;  APPLICANT:  Luca Rastelli
;  APPLICANT:  Mei Zhong
;  APPLICANT:  Muralidhara Padigaru
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
;  FILE REFERENCE: Cura 551 CIP
;  CURRENT APPLICATION NUMBER: US/11/217,997
;  CURRENT FILING DATE:  2005-08-31
;  PRIOR APPLICATION NUMBER: 10/453,372
;  PRIOR FILING DATE: 2003-06-03
;  PRIOR APPLICATION NUMBER: 10/055,877
;  PRIOR FILING DATE: 2002-01-22
;  PRIOR APPLICATION NUMBER: 60/262,892
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,598
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/263,799
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/264,117
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,139
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,478
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/263,351
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/272,870
;  PRIOR FILING DATE: 2001-03-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
;   LENGTH: 1577
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-217-997-16

  Query Match             4.9%;  Score 115.5;  DB 7;  Length 1577;
  Best Local Similarity   20.6%;  Pred. No. 0.13;
  Matches  124;  Conservative   36;  Mismatches  210;  Indels  231;  Gaps   35;

Qy         17 PGV-QALLCQFGTV-QHVWKVSDLPRQWTPKNTSCDS-------GLGCQDTLMLIESGPQ 67
              ||  |   || |    ||      |  |  : | |:        || |:       :|
Db        917 PGCEQRCQCQHGAACDHVSGACTCPAGW--RGTFCEHACPAGFFGLDCRSACN-CTAGAA 973

Qy         68 VSLVLSKGCTEAKDQEPRVTE---------HR-------------------------MG 92
                |       |  : ||  |         |                          ||
Db        974 CDAVNGSCLCPAGRRGPRCAESACPAHTYGHNCSQACACFNGASCDPVHGQCHCAPGWMG 1033

Qy         93 P--------GLSLISYTFVCRQEDFCNNLVNSLPL---------WAPQPPADPGSLRCPV 135
              |        ||    |   ||    | |     |:         ||          | | |
Db       1034 PSCLQACPAGL----YGDNCRHSCLCQNGGTCDPVSGHCACPEGWA--------GLACEV 1081

Qy        136 ----------CLSMEGCLEG------TTEEICPKGTT-----------------HCYDGL 162
                       |    ||| |      |   :|| | |                 || :|
Db       1082 ECLPRDVRAGCRHSGGCLNGGLCDPHTGRCLCPAGWTGDKCQSPAACAKGTFGPHC-EGR 1140

Qy        163 LRLRGG--------------------------GIFSNLRVQGCMPQPG--CNLLNGT-- 191
                | |                         | |     | |   ||  |: : |
Db       1141 CACRWGGPCHLATGACLCPPGWRGPHLSAACLRGWFGEACAQRCSCPPGAACHHVTGACR 1200

Qy        192 -----------QEIGPVGMTENCNRK-----DFLTCHRGTTIMT-----HGNLAQEPTDW 230
                        |    |    |:| :      :   ||  |   :     ||   |
Db       1201 CPPGFTGSGCEQACPPGSFGEDCAQMCQCPGENPACHPATGTCSCAAGYHGPSCQ----- 1255
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Qy        231 TTSNTEMCEVGQV---CQETLLLIDVGLTSTLVGTKGCST--VGAQNSQKTTIHSAPPGV 285
Db       1256 -----QRCPPGRYGPGCEQLCGCLNGGSCDAATGACRCPTGFLGTDCNL-----TCPQGR 1305

Qy        286 LVASYTHFCSSDLCNSASSSSVLLNS--LPPQAAPVPGDRQCP----------TC-VQPL 332
Db       1306 FGPNCTHVCG---CGQGAACDPVTGTCLCPPGRAGVRCERGCPQNRFGVGCEHTCSCRNG 1362

Qy        333 GTCSSGSPRMTCPRGAT--HC--------YDGYIHL--SGGGLSTKMSIQG-CVAQPSSF 379
Db       1363 GLCHASNGSCSCGLGWTGRHCELACPPGRYGAACHLECSCHNNSTCEPATGTCRCGPG-- 1420

Qy        380 LLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGV------GLALAPALWWGVV 433
Db       1421 ----------FYGQACEHPCPPG--FHGAGCQGLCWCQHGAPCDPISGRCLCPAGFHGHF 1468

Qy        434 C 434
Db       1469 C 1469
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Search completed: July 11, 2006, 09:35:15
Job time : 23 secs